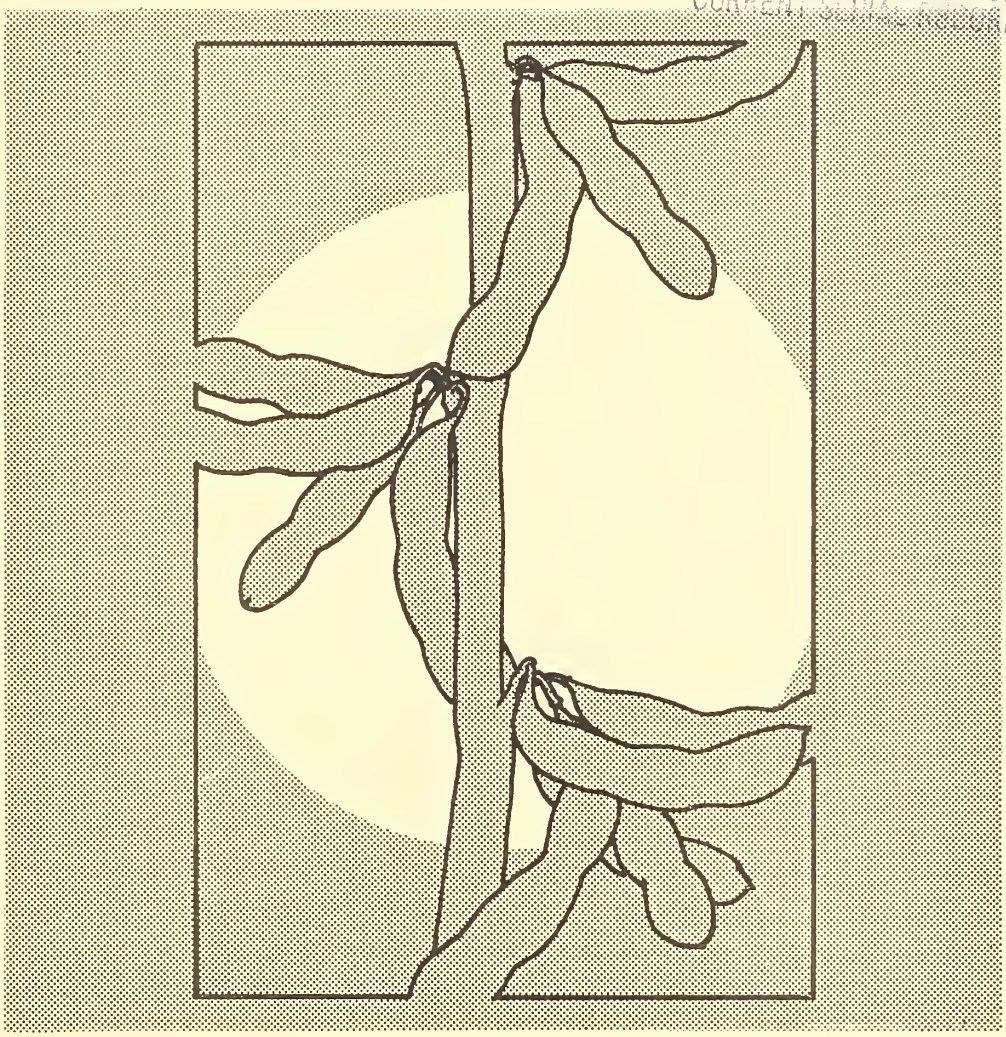
Soybean Genetics Newsletter



Volume 8 April 1981

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Agricultural Research Service-USDA
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I. FOREWORD

When the Soybean Genetics Newsletter was initiated in 1974, statistics available for the 23 major soybean producing countries of the world indicate that the area planted to soybeans totalled 39 million hectares. By 1979, that total has increased to 52 million hectares.

This expansion in the importance of soybeans is reflected in the continuing growth of the Soybean Genetics Newsletter. The Newsletter is mailed to more than 50 countries all around the world. Contributions of research notes come from many continents. The content of the research is indicative of the problems being encountered in the particular country represented. Middle European countries are striving to develop cultivars adapted to cool temperatures and shorter growing seasons. Southeastern Asian countries have severe problems with various virus diseases.

We think that the Newsletter, thanks to you the readers and contributing authors, is fulfilling its original purpose as a forum for exchange of ideas and "preliminary and speculative" reports on research.

Publication of the newsletter is no small task. Our sincere thanks go to Therese Curry, Peggy Hatfield, Holly Heer, Sally Pyle and Randy Shoemaker for their assistance with Volume 8.

Reid G. Palmer, editor

C. R. (Bob) Weber
1914 - 1980

II. IN MEMORIAM

Memorial to Dr. C. R. (Bob) Weber - July 18, 1914 - August 12, 1980

Billy E. Caldwell
North Carolina State University
Department of Crop Science
P. O. Box 5155
Raleigh, North Carolina 27650

Each of us leave our tracks in history and are remembered for our contributions to our profession. Certainly Bob Weber left big tracks during his years of service to the profession of plant breeding and genetics as a member of the USDA-ARS and as a member of the faculty of Iowa State University. Only those of us who knew him best knew the depth of feeling and commitment that he had for soybeans.

Bob Weber did not emerge all of a sudden as the dynamic individual whom I knew at Iowa State. Born in 1914 in Pana, Illinois and reared on a farm, his early life was characterized by hard work and the establishment of values that reflected the work ethic needed to survive the 1920s and 1930s. He did not move immediately into the academic life as is characteristic of most professionals today. He spent time as a farmer, commercial rose grower, and worked as a rural resettlement official for the USDA. He was 26 years old when he received his Bachelors degree from the University of Illinois, but then only a year later he received his Masters degree. Service in World War II interrupted his Ph.D. program. However, this did not deter his dedication and commitment, and he returned to Iowa State and received the Ph.D. in 1948. By the time he received his Ph.D. he had already begun to make his mark as a soybean breeder at Iowa State University.

Today, it is hard for us to visualize the role the scientist of Dr. Weber's era played in the improvement of our commodities. It is difficult for us to envision that soybeans, during Dr. Weber's early years, was a new crop -- a crop that had to be introduced and for which management techniques had to be learned. In essence, the plant breeder of that era had to be capable of dealing with the many facets of breeding, genetics, and crop production. In fact, at one time, Dr. Weber was classified as an Agronomist. It is also difficult for us to envision the stringency of research budgets after World War II, and the necessity for the researchers to do much of the work themselves, including

developing and maintaining the equipment. Those of us who knew Bob Weber can remember the many remnants of those early years that were retained because one of Bob's characteristics was never to throw anything away.

Only those who knew Bob well could know of his fiercely competitive spirit. His passion for excellence and to do better than the next individual permeated his whole life, whether it was breeding soybeans, hunting pheasants, or bowling. He was totally committed in everything he undertook. He firmly believed that nothing was worth doing if you were not willing to put the work, the sweat, into getting the job accomplished as it should be. The following quote was posted prominently above the graduate students' desks, and reflected Bob's philosophy. "The Father of success is Work. The Mother of success is Ambition. The eldest son is Common Sense. Some of the older boys are Perseverence, Honesty, Thoroughness, Foresight, Enthusiasm, Cooperation. The eldest daughter is Character. Some of the sisters are Cheerfulness, Loyalty, Courtesy, Care, Economy, Sincerity. The baby is Opportunity. Get acquainted with the old man and you will be able to get along pretty well with the rest of the family."

The outward appearance, the large hands, the big body, the swift and aggressive movement belied the sensitive person underneath. Again, only those who knew him best knew the sensitivity of this man. He was totally committed to soybeans, and he expected and often demanded a similar commitment from his graduate students and technicians. However, he quickly recognized when a student was unhappy or angry and took time to discuss the issue. In his own way he was concerned about people. But those of us who served as his graduate students can appreciate the support that he gave when the time came to write a thesis and to find a job. He truly had a sincere and intense desire to help the young make the transition from student to professional. His students have had and will continue to have an impact on soybean breeding and genetics and upon the growth of the industry in the world. So even though he is no longer with us, his work goes on.

There is no question in anyone's mind that Bob was an outstanding plant breeder, an authority and an expert on soybeans -- one of the best in the world. He had an in-depth and unique understanding of the genetic behavior of soybeans, and could see much more in a soybean plant than most any of us who worked with him. There is little question that Dr. C. R. Weber is one of the major reasons soybeans now occupy more than 8 million acres in Iowa. It was a

sad day for public research when Dr. Weber retired and took employment with private industry for his niche and role in life was in public research and in the training of students.

Any memorial to Dr. C. R. would be inappropriate without a brief comment about Peg, Ian, and Janie. A man as devoted as Bob was to his career had little time for family. But it was a joy to have an opportunity to have a glass of wine, a snack, or a meal at the Weber's home. Peggy was always a delightful hostess and the children were a joy to be around. They, too, were important to us who knew Bob best.

So the tracks are there and the direction is still clear for those of us who wish to make a contribution to agriculture. We need only to look at the dedication, devotion, and commitment to improvement that Bob had for soybeans and to try to follow them. Although we often remember straightening wires so that old tags could be reused, strings that were too short to use, and gathering stakes that seemed to be of no value, we realize that these habits came from a heritage of hard work, short budgets and long hours.

III. ANNOUNCEMENTS

Soybean Germplasm Advisory Committee

This committee was established by the Soybean Genetics Committee to serve the following functions:

1) To serve in an advisory capacity to the National Plant Germplasm Committee, to the Germplasm Resources Information Program, and to other national groups concerned with soybean germplasm.

2) To serve in an advisory capacity to the curators of the soybean germplasm collection and to promote and coordinate the worldwide procurement of soybean germplasm and programs concerning its maintenance, evaluation, and distribution.

3) To serve in an advisory capacity to research institutions, especially the USDA and the state agricultural universities, in fostering soybean germplasm programs.

The Committee consists of the curators and representatives of the evaluators and users of soybean germplasm. Current members, in addition to curators E. E. Hartwig and R. L. Bernard, are R. L. Nelson, USDA and University of Illinois, whose full-time assignment is germplasm evaluation and who is acting as chairman of the committee; M. J. Sullivan, entomologist at Clemson University; S. M. Lim, USDA pathologist at the University of Illinois; C. W. Jennings, breeder with Pioneer Hi-Bred International in Iowa; J. W. Lambert, breeder at the University of Minnesota; and C. Williams of Jacob Hartz Seed Company in Arkansas.

National Plant Genetic Resources Board

The National Plant Genetic Resources Board, which has responsibility for providing advice on national policies for soybeans, requested that three individuals in soybean research be designated as contact persons. Those selected by the Soybean Genetics Committee to serve in this capacity are: T. Hymowitz representing State Agricultural Experiment Stations, J. R. Wilcox representing USDA-SEA, and H. B. Collins representing private industry.

SOYBEAN RUST NEWSLETTER

The fourth volume of the Soybean Rust Newsletter is being published by International Working Group on Soybean Rust and will be available in April 1981. Single copies of the newsletter can be obtained free by writing to:

Mr. S. Shanmugasundaram
Secretary, IWGSR
AVRDC, P. O. Box 42
Shanhua, Tainan 741, Taiwan
REPUBLIC OF CHINA

Request for contributions to the fifth issue of "Soybean Rust Newsletter"

Research articles, reports, notes, announcements of resistant or tolerant germplasm, and any other news item related to soybean rust are requested, and they will be accepted until December 31, 1981. Address all correspondence regarding the SRN to the above address.

Rules for contributions

1) Information in the SRN will be informal to stimulate the exchange of ideas and information among soybean rust scientists. SRN articles may be preliminary in nature and speculative in content, and should not be regarded as equivalent to papers published in formal scientific journals. Even so, such reports can be very valuable and helpful, if viewed in the proper perspective. Data presented in the SRN are not to be used in other publications without the consent of the respective authors.

2) Contributions should be in English, typed double spaced on 8½" by 11" pages. You may send as many separate contributions as you wish. Send two copies for each article.

3) Correspondence regarding an article should be on a separate page.

4) Photographs should be glossy black/white prints of high quality with good dark and light contrasts. Drawings for graphs and charts should be prepared with India ink on good quality tracing paper. Typewritten matter is not usually acceptable on graphs and charts. A good size for photographs is 5" by 7" and drawings is what will fit on an 8½" by 11" page.

5) Except for possible minor editing, manuscripts will be published as received from contributors.

6) Title your report, place your name(s), name of university, institution or company under the title. Please give complete address. (For contributors outside Taiwan (R.O.C.), please send reports by airmail.)

7) Citations of recent publications on soybean rust are specifically solicited.

8) Your participation in SRN will be greatly appreciated

New Officers for Commercial Soybean Breeders Association

Chairman:
Dr. Harry B. Collins
Delta & Pine Land Co.
Scott, MS 38772
(601) 742-3351

Vice-Chairman:
Dr. John D. Hicks, Jr.
Dept. Soybean Breeding
Plant Breeding Division
Pioneer Hi-Bred International, Inc.
Box 916, Leland, MS 38756
(601) 686-2211

Secretary-Treasurer:
Dr. Wayne Ellingson
Agri-Pro
Box 1668
Ames, IA 50010
(515) 232-0691

IV. REPORT OF THE SOYBEAN GENETICS COMMITTEE

A) The current members of this committee and the expiration dates of their terms are as follows:

R. L. Bernard, USDA (1982)
Turner Hall
Department of Agronomy
University of Illinois
Urbana, IL 61801

R. I. Buzzell (1984)
Agriculture Canada
Research Station
Harrow, Ontario
Canada NOR 1GO

T. E. Devine, USDA (1982)
CCNFL, Bldg. 001
BARC-West
Beltsville, MD 20705

E. T. Gritton, Chairman (1983)
Department of Agronomy
University of Wisconsin
Madison, WI 53706

H. H. Hadley (1984)
Turner Hall
Department of Agronomy
University of Illinois
Urbana, IL 61801

R. G. Palmer, USDA (Ex-Officio)
(Editor, Soybean Genetics Newsletter)
Department of Genetics
Iowa State University
Ames, IA 50011

C. Newell (1983)
Turner Hall
Department of Agronomy
University of Illinois
Urbana, IL 61801

B) Organization of the Committee:

1) The Committee will be composed of six elected members and the editor of the Soybean Genetics Newsletter.
2) The term of the elected members will be three years. After a member has been off for one year, he (she) can be reelected. The Committee will elect two new members each year; a simple majority is needed for election. The members will be elected prior to February 1 of each year, by a mail ballot conducted by the chairman.
3) At the annual meeting of the Committee (usually in February in conjunction with the Soybean Breeding and Genetics Workshop), the two new members and the two retiring members of the Committee are eligible to attend and vote.
4) The chairman will be elected at the annual Committee meeting and serve through the next annual meeting, and may be reelected.

C) The duties of this Committee include the following:

1) Maintain Genetic Collection.

The Genetic Collection is divided into four categories:

a) Type Collection includes all published genes of soybeans, preferably in the original strains (excluding U.S. and Canadian name varieties, which are maintained in a separate collection) plus certain mutants or strains that appear to the Committee to have potential genetic interest.

b) Isoline Collection includes adapted varieties Clark, Harosoy and Lee, into which have been backcrossed single genes or combinations of genes. Also included are certain genes or combinations with Chippewa, Wayne and Williams.

c) Linkage Collection includes linkage combinations and the various genetic recombinations.

d) Cytological Collection includes translocations, inversions, deficiencies, trisomics, tetraploids, etc.

Collections a, b and c are maintained at Urbana, Illinois, with R. L. Bernard as curator. Collection d is maintained at Ames, Iowa, with R. G. Palmer as curator.

2) Manuscript review and genetic symbol approval.

The Soybean Genetics Committee requests that researchers submit all manuscripts concerning qualitative genetic interpretation and symbols to the Committee Chairman. This review by the Genetics Committee will serve to insure orderly identification and use of genetic nomenclature and to avoid conflict of symbols. This will also allow assignment of type collection designations (T-numbers) prior to publication, so that these T-numbers may be used in the journal article to identify parental lines.

3) Soybean Genetics Newsletter notes.

All notes for the Newsletter should be sent to the SGN editor, R. G. Palmer, who will ask the Soybean Genetics Committee to review those articles concerning qualitative genetic interpretation and symbols. Genetic symbols reported in the Newsletter will have the same status as those published in scientific journals.

D) The Committee will take the responsibility for publishing every five years, starting in 1982, in the SGN a list of all gene symbols, linkage groups, translocations, and trisomics in soybeans. Researchers who have references on the gene symbols and linkage groups are urged to send them to R. L. Bernard or T. Hymowitz. Researchers who have references on translocations and trisomics are urged to send them to R. G. Palmer.

E) The function of the Committee was officially expanded to include genetics research in the entire *Glycine* genus rather than restricting its responsibilities to *Glycine max*.

F) Researchers submitting manuscripts on new gene symbols are urged to furnish R. L. Bernard with seeds of the line carrying the reported gene. From 50 seeds to 300 gms of seed of each line are needed to maintain the genetic type collection. When these seeds are received, the genetic type number can be assigned and can then be reported by the author in a manuscript.

Rules for Genetic Symbols

I) Gene Symbols

a) A gene symbol shall consist of a base of one to three letters, to which may be appended subscripts and/or superscripts as described below.

b) Genes that are allelic shall be symbolized with the same base letter(s) so that each gene locus will be designated by a characteristic symbol base.

c) The first pair of genes reported for a gene locus shall be differentiated by capitalizing the first letter of the symbol for the dominant or partially dominant allele. (Example: *Ab*, *ab*. *Ab* is allelic and dominant to *ab*.) If genes are equivalent, codominant, or if dominance is not consistent, the capitalized symbol may be assigned at the author's discretion.

d) When more than two alleles exist for a locus, the additional alleles or those symbolized subsequently to the pair first published shall be differentiated by adding one or two uncapitalized letters as a superscript to the base. (Example: R, r^m, r.) This shall be the only use of superscripts. The base for the additional alleles is capitalized only

when the gene is dominant or equivalent to the allele originally designated with a capitalized symbol. The superscript may be an abbreviation of a descriptive term. When allelism is discovered for a gene previously assigned a symbol, the previous symbol may be used as the superscript.

e) Gene pairs with the same or similar effects (including duplicate, complementary, or polymeric genes) should be designated with the same letter base differentiated by numerical subscripts, assigning 1, 2, 3, 4, etc., consecutively in the order of publication. (Example: The *y* series for chlorophyll deficiency.) This shall be the only use of subscripts. Letter subscripts should not be used. The subscript 1 is automatically a part of the first reported gene symbol for each base but may be omitted until the second symbol is assigned.

f) Base letters may be chosen so as to indicate apparent relationships among traits by using common initial letters for all loci in a related group of traits. Examples are *P* for pubescence type, *R* for disease reaction (plus two initials of the pathogen to complete the base), and *L* for leaf shape.

g) The distinction between traits that are to be symbolized with identical, similar, or with unrelated base letters is necessarily not clear cut. The decision for intermediate cases is at the discretion of the author but should be in accordance with previous practices for the particular type of trait. The following sections concern supplementary symbols that may be used whenever desired as aids to presentation of genetic formulas.

h) A dash may be used in place of a gene symbol to represent <u>any</u> allele at the indicated locus. The locus represented should be apparent from its position in the formula. (Example: *A*_ represents both *AA* and *Aa*.)

i) A question mark may be used in place of a symbol when the gene is unknown or doubtful, or it may be used as a superscript to the base symbol for the same purpose. (Example: $a^{?}$ indicates that the latter is an unknown allele at the *A* locus.)

j) Plus symbols may be used in place of the assigned gene symbols of a designated standard homozygous strain when this will facilitate present-

ing genetic formulas. The standard strain may be any strain selected by the worker, as long as the strain being used and its genetic formula are made explicit.

II) Linkage and Chromosome Symbols

a) Linkage groups and the corresponding chromosomes shall be designated with Arabic numerals. Linkage shall be indicated in a genetic formula by preceding the linked genes with the linkage group number and listing the gene symbols in the order that they occur on the chromosome.

b) Permanent symbols for chromosomal aberrations shall include a symbol denoting the type of aberration plus the chromosome number(s) involved. Specific aberrations involving the same chromosome(s) shall be differentiated by a letter as follows: The symbol Tran shall denote translocations. Tran 1-2a would represent the first case of reciprocal translocations between chromosomes 1 and 2, Tran 1-2b the second, etc. The symbol Def shall denote deficiencies, Inv inversions, and Tri primary trisomics. The first published deficiency in chromosome 1 shall be symbolized as Def 1a, the second as Def 1b, etc. The first published inversion in chromosome 1 shall be denoted as Inv 1a, etc. The first published primary trisomic shall be designated with the Arabic numeral that corresponds to its respective linkage group number.

c) Temporary symbols for chromosomal aberrations are necessary, as it may be many years before they are located on their respective chromosomes. Tran 1 would represent the first case of a published reciprocal translocation; Tran 2, the second case, etc. The first published deficiency shall be symbolized as Def A, the second as Def B, etc. The first published inversion shall be symbolized as Inv A, and second as Inv B, etc. The first published primary trisomic shall be designated as Tri A, the second as Tri B, etc. When appropriate genetic and/or cytological evidence is available, the temporary symbols should be replaced with permanent symbols, with the approval of the Soybean Genetics Committee.

III) Cytoplasmic Factor Symbols

a) Cytoplasmic factors shall be designated with one or more letters prefixed by cyt-. (Example: *cyt-G* indicates the cytoplasmic factor for maternal green cotyledons, *cyt-Y* indicates that for maternal yellow cotyledons.)

IV. Priority and Validity of Symbols

a) A symbol shall be considered valid only when published in a recognized scientific journal, or when reported in the Soybean Genetics Newsletter, with conclusions adequately supported by data which establish the existence of the entity being symbolized. Publication should include an adequate description of the phenotype in biological terminology, including quantitative measurements wherever pertinent.

b) In cases where different symbols have been assigned to the same factor, the symbol first published should be the accepted symbol, unless the original interpretation is shown to be incorrect, the symbol is not in accordance with these rules, or additional evidence shows that a change is necessary.

V) Rule Changes

a) These rules may be revised or amended by a majority vote of the Soybean Genetics Committee.

V. USDA SOYBEAN GERMPLASM REPORT

More than 1700 lines have been added to the soybean germplasm collection (North and South) in 1980. These entries are from Korea (8), China (20), and the USSR (1708) and greatly increase the number of lines available in Maturity Groups 000 to II. The introductions received from the USSR were from the soybean collection at the Vavilov Institute of Plant Industry in Leningrad. These lines represent 21 different regions of the USSR and 29 other countries including more than 700 lines originally from China. The distribution of these lines by maturity groups is as follows:

000	11
00	106
0	378
I	615
II	447
III	107
IV	53
later than IV	19
TOTAL	1736

These are preliminary totals and the final numbers may differ slightly.

A complete numerical list of soybean introductions including origin, foreign variety name, any other information received with the introduction, and our maturity group classification has been completed for the period 1900-1977. It is currently being reviewed and should be available for general distribution within a year. Final publication is being delayed so that maturity groups can be confirmed with data from the agronomic evaluation currently being conducted. Table 1 is from that document and summarizes the origins of the entries in the PI Collection through 1977. Table 2 is a summary by maturity group which gives a current count on the total number of introductions in the Collection. Table 3 is a chronological history of the growth of the Collection.

One year of the general agronomic evaluation of northern germplasm has been completed. These tests include all PI's from 273,483 through 427,107 in Maturity Groups 000-IV. Group 0 and earlier are being grown by Dr. Jean Lambert in Minnesota and the late Group IV lines are being grown by Dr. James Orf in Kentucky. In total, 2,770 lines are being evaluated. This data will be available late in 1982.

Table 1.

Number of strains in the PI collection by country
+ number in the variety collection
(Introduced 1900 to 1977, to PI 420,338)

	Total	Maturity Group 000 to IV	Maturity Group V to X
Asia			
Afghanistan	5	0	5
Burma	3	0	3
China	1039+79	949+56	90+23
India	228	2	226
Indonesia	16	0	16
Iran	1	1	0
Israel	13	7	6
Japan	1543+32	961+28	582+4
Korea	2242+19	1251+11	991+8
Malaysia	30	0	30
New Guinea	1	0	1
Nepal	24	0	24
Pakistan	15	0	15
Philippines	18	0	18
Taiwan	26	2	24
Thailand	34	0	34
Turkey	6	5	1
Vietnam	5	0	5
PI Total	5249	3178	2071
Variety Total	130	95	35
Africa			
Algeria	1	1	0
Angola	7	0	7
Cameroun	2	0	2
Kenya	3	0	3
Liberia	1	0	1
Mozambique	6	0	6
Sierra Leone	1	0	1
South Africa	32	0	32
Sudan	3	0	3
Tanzania	7	0	7
Uganda	31	0	31
Zaire	2	0	2
Zimbabwe	5	0	5
Total	101	1	100
Australia			
Australia	31	7	24

	Total	Maturity Group 000 to IV	Maturity Group V to X
Europe			
Austria	2	2	0
Belgium	88	88	0
Bulgaria	44	44	0
Czechoslovakia	6	6	0
England	1	1	0
France	101+2	101+2	0
Germany	37	37	0
Hungary	102	102	0
Italy	0+1	0+1	0
Netherlands	21	21	0
Poland	8	8	0
Portugal	3	3	0
Romania	143	143	0
Sweden	56	56	0
USSR	107+5	106+5	1
Yugoslavia	24	24	0
PI Total	743	742	1
Variety Total	8	8	
North America			
El Salvador	3	0	3
Guatemala	3	0	3
United States	4	0	4
Total	10	0	10
South America			
Argentina	7	1	6
Brazil	15	0	15
Colombia	5	0	5
Peru	8	1	7
Surinam	14	0	14
Uruguay	5	5	0
Venezuela	9	0	9
Total	63	7	56
Misnumbered	37	31	6
PI TOTAL	6234	3966	2268
VARIETY TOTAL	138	103	35

Table 2.

Number of strains in the USDA Soybean Germplasm Collection by Maturity Group

Maturity Group	FC	PI to 1944	PI 1944-1977	PI After 1977	PI Total
000	1	0	49	15	64
00	4	4	169	117	290
0	6	7	343	394	744
I	3	93	288	641	1022
II	6	404	248	480	1132
III	13	428	402	165	995
IV	18	320	1211	576	2107
North	51	1256	2710	2388	6354
V	10	71	1124	150	1345
VI	10	39	299	56	394
VII	17	14	251	8	273
VIII	2	3	226	10	239
IX	0	0	101	8	109
X	0	0	140	0	140
South	39	127	2141	232	2500
Total	90	1383	4851	2620	8854

Table 3.

A statistical history of soybean introduction

Period	Years	Rate	Number of Soybean PI Numbers	Current Number of Strains	
				PI Coll'n	Variety Coll'n
1898-1923	26	40/yr	1053	51	81
1924-1928	5	375/yr	1878	287	16
1929-1932	4	1193/yr	4773	1010	41
1933-1944	12	14/yr	169	35	0
1945-1974	30	85/yr	2555	2094	0
1975-1977	3	843/yr	2529	2757	0
Total	80	162/yr	12,957	6234	138

The germplasm lists and reports below are available from

Dr. R. L. Bernard, USDA
Turner Hall - Agronomy
University of Illinois
Urbana, IL 61801

except that those marked with an asterisk are available from

Dr. E. E. Hartwig, USDA
Delta Branch Experiment Station
Stoneville, MS 38776

Requests for seeds in Maturity Groups IV or earlier should be addressed to Dr. Bernard and requests for seeds in Maturity Groups V and later should be addressed to Dr. Hartwig.

Checklists giving name and Maturity Group (extra copies available to use in making requests for large number of strains):

1) Checklist of U.S. and Canadian varieties (00 to IV), January 1980.
2) Checklist of FC and PI strains (00 to IV), January 1980.
*3) Checklist of varieties and FC and PI strains (V to X), 1980.

Evaluation reports giving origin of strains and descriptive, agronomic, and seed composition data:

1) Varieties, Groups 00 to IV, 1970.
2) Varieties and FC and PI strains, Groups 00 to 0, 1965.
3) Varieties and FC and PI strains, Groups I to II, 1966.
4) Varieties and FC and PI strains, Groups III to IV, 1969.
*5) Varieties and FC and PI strains, Groups V to X, 1975.
*6) Evaluation II, PI Strains, Groups V to X (PI 330,635 to 424,616), 1980.

List of Genetic Type Collection, Aug. 1979.

List of backcross isolines of Clark and Harosoy, 1975.

List of wild soybeans, *Glycine soja*, 1979.

List of Perennial *Glycine* accessions, June 1979.

R. L. Bernard
Research Geneticist

R. L. Nelson
Research Geneticist

VI. RESEARCH NOTES

ALABAMA A&M UNIVERSITY
Department of Natural Resources
Normal, AL 35762

1) Screening soybeans for cyst nematode (*Heterodera glycine*).

Twelve soybean strains from MG V supplied by Dr. E. E. Hartwig, and four other cultivars ['Lee' (MG VI), 'Pickett 71' (MG VI), 'Davis' (MG VI) and 'Ransom' (MG VII)] were included. 'Essex', as susceptible, and 'Forrest', as resistant, also were included. The experimental area was fertilized with 412 kg/ha of P_2O_5 and K_2O and 4.0 tons/ha of calcitic lime was applied to raise the soil pH to 5.7. A total of 16 cultivars was planted in a 4-row plot on June 2, in a cyst nematode (*Heterodera glycine*) race 3-infested field in a randomized complete block design with three replications.

At different growth stages, 50 cc of soil around roots (10-25 cm diameter, 20-25 cm deep) was collected. The number of cysts per 50 cc and the number of nodules per plant were counted. However, drought stress was quite severe in the spring of 1980, and, as a result, number of cysts and number of nodules at fourth and seventh trifoliolate stages did not show good difference between the resistant and susceptible soybeans. But at a later stage, eleventh trifoliolate, and at maturity, there was good difference between soybean strains (Table 1). Cultivars Lee, Davis, Ransom showed similar reaction to Essex, a susceptible cultivar while other strains showed similar reaction to Forrest, which is resistant to race 3 (Table 1).

Val T. Sapra
T. Mebrahtu
Athel Aljeleli

Table 1

Number of cysts and nodules per plant[1] at different stages of soybean lines

Cultivar	4-Trifoliolate		7-Trifoliolate		11-Trifoliolate		Maturity		Season average	
	Number of		Number of		Number of		Number of		Number of	
	Cysts	Nodules	Cysts	Nodules	Cysts	Nodules	Cysts	Nodules	Cysts	Nodules
Essex	18.4	11.4	20.2	4.9	47.1	8.1	40.2	8.4	31.5	8.2
Forrest	11.2	12.5	7.1	10.7	12.2	14.2	11.9	14.3	10.6	12.9
Ransom	11.2	6.5	32.5	4.7	56.5	4.8	47.2	7.1	36.9	5.8
Davis	3.8	12.0	14.9	4.2	36.1	6.3	29.3	6.9	21.0	7.3
Lee	11.2	11.6	19.9	6.2	39.3	5.1	34.4	6.8	26.2	7.4
Bedford	4.5	18.5	3.2	14.2	11.3	18.2	5.7	19.2	6.2	17.5
D77-3008	6.2	15.2	3.3	13.2	9.9	17.6	9.1	19.5	7.1	16.4
D77-5169	6.3	7.6	6.4	11.3	11.0	11.9	8.5	10.2	8.0	10.2
J74-51	6.9	6.6	2.9	14.0	5.3	20.9	4.5	19.2	4.9	15.2
D77-5090	3.6	8.9	4.3	11.2	12.6	12.3	13.5	19.4	8.5	12.9
D77-8	3.4	13.7	2.5	17.5	7.4	15.6	5.9	17.4	4.8	16.1
D78-3100	4.7	12.8	4.2	11.9	12.7	14.0	9.9	13.1	7.9	12.9
D78-3110	3.9	12.0	7.0	8.7	11.1	15.2	8.5	20.1	7.6	22.8
D77-4874	5.0	9.3	3.5	12.2	12.0	15.3	8.1	16.0	7.1	13.2
D78-3052	3.2	8.4	5.9	13.6	13.1	14.5	8.9	18.1	7.8	13.6
Pickett 71	5.2	10.6	16.5	3.6	12.7	11.7	10.0	10.5	11.1	9.1

[1]Cysts per 50 cc of soil and nodules per plant.

2) Leaves as a source of somatic chromosomes for cytogenetic studies of soybean.

The cytogenetic study of soybean [*Glycine max* (L.) Merr.] is difficult because of the physical properties of the chromosomes, i.e., size and number. In addition, the radical is thick and must be split in order to obtain proper penetration of treatment fluids. This is a tedious procedure and still requires eventual enzyme treatment to soften the root tip for effective squashing. This process paper tells how very young leaves are used as a source of mitotic figures.

Procedure

1. Germinate seeds on wet filter paper in Petri dishes for 3 to 4 days at room temperature and light.
2. Split cotyledons apart; remove the primary leaf and refrigerate in a saturated, aqueous solution of paradichlorobenzene for 24 hours.
3. Fix leaves in 45% aceto-orcein for a minimum of one week.
4. Hydrolyze leaves in HCl-aceto-orcein (1 part 2N HCl to 9 parts 45% aceto-orcein) for 2 hours. Rinse in distilled water and return leaves to 45% aceto-orcein.
5. Place a small portion of leaf on a slide in a drop of 45% acetic acid and macerate thoroughly. Apply a coverslip, tap repeatedly and squash thoroughly using a slide press.

Discussion An abundance of metaphase cells was obtained without cycling the temperature and light in a controlled environment. The most active mitosis was observed when leaves were 2 to 3 mm in length and secondary roots were just beginning to emerge. An extended fixation time proved advantageous in obtaining well-flattened cells. Leaves frozen in aceto-orcein for 2 to 3 weeks prior to hydrolysis gave excellent results (photographs). Avoiding the use of enzymes gave a clearer preparation with well-defined chromosomes. Satisfactory results could not be obtained using leucobasic fuchsin or carbol fuchsin.

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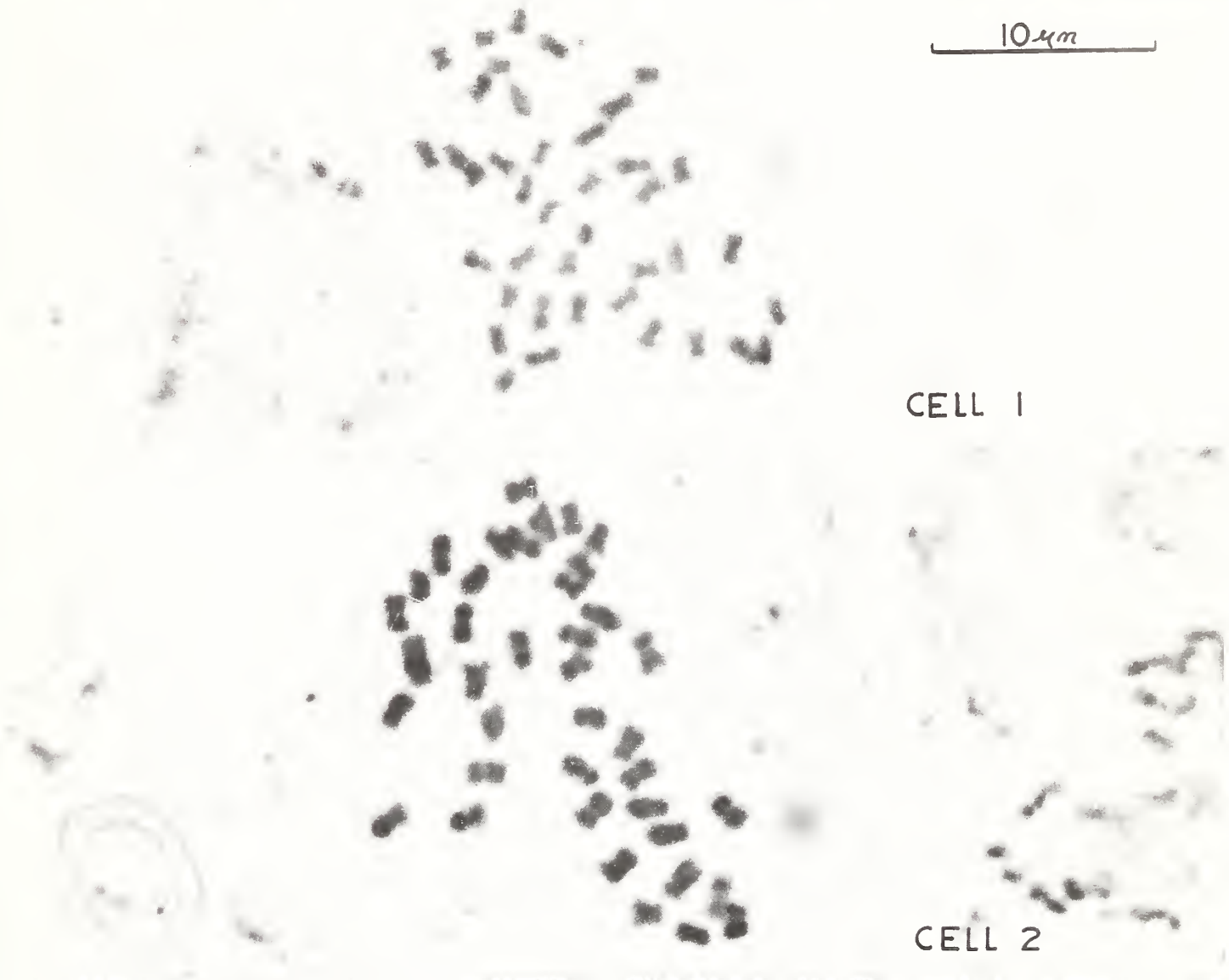
10μm
CELL 1
CELL 2


CELL 3

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1) Resistance of soybean lines and cultivars to the root-knot nematode, *Meloidogyne javanica*.

In a clayed soil heavy infested with *Meloidogyne javanica* at Guatapará farm, state of São Paulo, 36 soybean cultivars and breeding lines were tested for resistance to this nematode. Plots were constituted of three rows, 3 m long and 0.60 m apart and each plot was bordered on both sides with a row of 'Davis' cv, the susceptible check. Soybeans were seeded in November, 1979, in a randomized complete block design with eight replications.

Root samples were taken 55 and 86 days after planting from the two external rows of each plot and from each check row, and infestation results were compared to the nearest Davis row (Arruda, 1952). Root galling was rated on a scale 1 to 5, where 1 = no galls in the roots and 5 = severe infestation (Lordello, 1976). The center row was used to determine seed yield.

As presented in Table 1, some lines showed more resistance to the nematodes than did the check Davis, and it is interesting to observe that the ten most resistant lines came from crosses in which IAC-2 cultivar was used.

The resistance showed by IAC-2 cultivar is probably similar to that of 'Hampton', cited by Good (1973), as moderately resistant to *M. javanica*. This similarity may lie in the fact that these cultivars have a common parent.

Since it was a rainy year, it was not possible to correlate seed yield to nematode attack (Table 2). New tests are being carried out since November, 1980.

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Table 1

Gall ratings of soybean lines and cultivars

Lines/ Cultivars	Gall ratings $\bar{X}$	Genealogy
IAC 78-1005	2.28	B-5 (IAC-2 x Clark 63 + Harosoy 63 x IAC-2
IAC 78- 958	2.29	B-5
IAC 78- 975	2.34	B-5
IAC 78- 982	2.37	B-5
IAC 78-1021	2.51	B-5
IAC 78- 971	2.64	B-5
IAC 78-1014	2.67	B-5
IAC 78- 988	2.69	B-5
IAC 78- 986	2.72	B-5
IAC 78- 939	2.73	Paraná x IAC 73- 231
IAC 78- 973	2.75	B-5
IAC 77- 655	2.82	Paraná x IAC 73- 231
IAC 78-1013	2.84	B-5
IAC 78- 962	2.92	B-5
IAC 78- 918	2.95	Paraná x IAC 73-231
IAC 78- 994	2.96	B-5
Paraná	2.97	Paraná
IAC 78- 998	3.02	B-5
IAC 78- 909	3.09	Vicoja x X-10
Foscarin-31	3.10	Foscarin-31
IAC 77- 407	3.18	Vicoja x X-10
IAC 78- 904	3.23	Vicoja x X-10
IAC 79- 344	3.28	Paraná x Vicoja
IAC 78- 952	3.32	Vicoja x F_1(Kanrich x Vicoja)
IAC 78- 876	3.38	Paraná x Vicoja
IAC 78- 922	3.47	Paraná x IAC 73- 231
IAC 78- 963	3.48	B-5
IAC 78- 992	3.50	B-5
IAC 78- 341	3.51	Paraná x Vicoja
IAC 78- 991	3.54	B-5
Holambra LM	3.55	
IAC 78- 589	3.56	Paraná x F_1(Davis x IAC 73-1364)
IAC 78- 927	3.64	Paraná x IAC 73- 231
IAC 79- 334	3.72	Paraná x Vicoja
IAC 78- 901	4.15	Vicoja x X-10
IAC 79- 350	4.49	Paraná x Vicoja
Davis	3.55	

Rate 1 = Without infestation
Rate 2 = Very light infestation
Rate 3 = Light infestation
Rate 4 = Moderate infestation
Rate 5 = Severe infestation

Table 2

Seed yield of soybean lines and cultivars

Lines/ cultivars	Seed yield (kg/ha) $\bar{X}$
Paraná	1146
Foscarin-31	1375
IAC 78-1021	1938
IAC 78- 998	2022
Holambra LM	1896
IAC 78- 918	2063
IAC 78- 927	2292
IAC 78- 991	1646
IAC 78- 973	1730
IAC 78- 986	917
IAC 78- 922	844
IAC 78-1031	1980
IAC 78- 876	1480
IAC 78-1005	1313
IAC 78- 909	1521
IAC 78- 982	1396
IAC 78- 939	1313
IAC 78- 963	1438
IAC 78- 962	1355
IAC 78- 975	1167
IAC 78-1014	1667
IAC 78- 994	1709
IAC 78- 971	1334
IAC 78- 988	1251
IAC 78- 952	1313
IAC 78- 992	1563
IAC 78- 901	1688
IAC 78- 904	1501
IAC 78- 958	1313
IAC 79- 341	1480
IAC 79- 350	1917
IAC 79- 334	1522
IAC 79- 344	1834
IAC 77- 407	1438
IAC 77- 589	2188
IAC 77- 655	1605

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1) Soybean tissue culture.

The recently developed techniques of plant tissue culture have been used to develop somatic cell genetics programs in solanaceous species, particularly *Petunia, Nicotiana,* and *Datura* (Vasil et al., 1979). Development of tissue culture techniques has permitted the isolation of biochemical mutants, production of somatic hybrids, and recovery of haploid plants. Unfortunately, extrapolation of these techniques to leguminous and graminaceous species of greater economic importance has proven quite difficult. Recent reports of plant regeneration from protoplasts of alfalfa, a legume (Kao and Michayluk, 1980) and pearl millet, a cereal (Vasil and Vasil, 1980), suggest that development of tissue culture techniques may be feasible for the more recalcitrant legumes such as soybean. This note is a summary of recent research in our laboratory with soybean tissue culture.

A. Plant regeneration Explants for plant regeneration experiments were derived from the albino soybean, y_{11}/y_{11}, and from the Canadian soybean cv. 'Maple Arrow'. All attempts to regenerate plants from mature leaf or stem segments of soybean have been unsuccessful. However, multiple shoot formation was induced from cultured cotyledon axillary bud explants. Axillary buds were excised from sterile 6-14-day-old seedlings from seeds sown on 10 g/l agar. Single bud explants placed on either Medium 1 or 2 (Table 1) produced a mean of 5 shoots per explant within 4 wks. Shoots could be separated and transferred to Medium 3, the soybean high rooting medium (HRM) published earlier (Evans et al., 1976), and each shoot transferred to HRM produced roots within 2 wks. Rooted plantlets of Maple Arrow then were transferred to the greenhouse where each plant grew to maturity. Chromosomes were counted in root tips of five regenerated plants and each contained 2n=40 chromosomes. This method of plant regeneration does not permit large scale plant propagation from mature explants, but will permit production of up to 10 plants from explants derived from a single seedling.

B. Cell suspension cultures Callus was initiated from hypocotyl sections of 9-day-old seedlings cultured on Medium 4. After 4 wks a friable white callus was obtained. Callus was transferred to a 60 X 15 mm disposable plastic Petri dish containing 3 ml of liquid culture Medium 5, and shaken at

Table 1

Culture media used for soybean experiments

Medium	Value
MS + 740 µM Ade 1 µM 6BA 0.1 µM NAA	multiple shoot formation from dormant cotyledon
MS + 740 µM Ade 1 µM 6BA 0.1 µM IBA	axillary buds
MS + 11 µM NAA 2 µM KIN 16 µM NicoA	root formation
MS + 1 µM KIN 1 µM IBA	callus formation for initiation of stable suspension culture
MS + 1 µM 2,4-D	maintenance of suspension cultures

MS = Murashige and Skoog (1962) macro and micronutrients with Gamborg B5 vitamins (Gamborg, 1975).

50 rpm. Three ml of fresh liquid Medium 5 were added 7 days after culture initiation. Four days later, the culture was transferred to a 250 ml flask with 20 ml of Medium 5. Afterwards cells were subcultured into new Medium 5 every 4 days. Cells from suspension cultures were prepared for chromosome counts as described (Evans and Reed, 1980), using cells 24 hrs after subculture. Cell suspension cultures with stable chromosome number, 2n = 40, were produced and maintained from both y_{11}/y_{11} albino soybean and Maple Arrow.

C. Plant protoplasts Protoplasts were readily isolated from the soybean suspension cultures 3 days after each subculture. Two ml of suspension culture were mixed with 2 ml of a protoplast isolation solution containing 2% Onozuka R10 (Kinki Yakult), 1% pectinase (Sigma), and 1% hemicellulase (Rohm and Haas) dissolved in 0.7 M glucose, 3 mM MES buffer, 6 mM $CaCl_2$, and 0.7 mM NaH_2PO_4 at pH 5.5. This mixture was incubated in the dark at room temperature and shaken at 50 rpm. Protoplasts were released in 6-8 hrs. Cellular debris was removed by filtration through a 44 µm filter, followed by centrifugation

twice at 100 g. Protoplasts were resuspended, then cultured in Medium 8p of Kao and Michayluk (1975). The protoplasts reformed cell walls within 24 hrs of transfer to culture medium and divided by day 2. A large fluffy white callus was produced from each soybean protoplast culture, but plant regeneration from this callus has not occurred to date.

Development of a cellular genetics system with soybean is limited by the present inability to regenerate intact plants from single cells. The work reported here suggests that most other techniques useful for plant somatic cell genetics, i.e., callus culture, cell suspension culture, and protoplast isolation and culture are similar to previously reported species and can be exploited without difficulty. Hopefully more efficient methods of plant regeneration will be achieved in the near future.

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1) Another major gene for resistance to *Phytophthora megasperma* var. *sojae* in soybeans

L62-904 has resistance (Table 1) to some races of *Phytophthora megasperma* var. *sojae* (*Pms*). L62-904 was developed by Dr. R. L. Bernard at Urbana from Harosoy^{6} x T240; it was an F_2 selection from an F_1 - BC_5 plant that was *Ps ps* W_1 w_1. It was used at Harrow as a w_1w_1 'Harosoy' isoline with white flowers/green hypocotyls as a genetic marker in crosses before it was discovered to have *Pms* resistance. The origin of parents used in crosses to L62-904 is given in Table 2.

Results (Tables 3, 4 and 5) indicate that L62-904 carries a single gene for resistance and that this gene is not at the Rps_1, Rps_3 and Rps_4 loci. Also, it is not at the locus of the gene in 'Altona' and the gene in 'Kingwa'. The symbol Rps_5 is proposed for the L62-904 gene. Rps_5 could be at the Rps_2 locus but there is no proof that Rps_3 (Mueller et al., 1978) and Rps_4 (Athow et al., 1980) are not at Rps_2 either.

Acknowledgment

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Table 1

Disease reactions of soybeans in response to races of *Pms*

	Race							
	1	2	3	4	5	6-7	8	9
L62-904	R	R	R	R	R	S	R	R
Rps_1	R	R	S	S	S	S	S	S
$Rps_1{}^b$	R	S	R	R	R	R	R	R
$Rps_1{}^c$	R	R	R	S	S	R	R	R
Rps_2	R	R	R	R	R	S	S	R
Rps_3	R	R	R	R	R	S	R	R
Rps_4	R	R	R	R	S	S	S	S
Altona - Rps	R	R	R	R	S	S	S	S
Kingwa - Rps	R	R	R	R	R	R	R	R

R = Resistant S = Susceptible

Table 2

Parents used in crosses with L62-904

	Genes
Harrow lines	
OX693: Harosoy 63 x Altona	"Altona - Rps"
OX696: Harosoy x Kingwa	"Kingwa - Rps"
OX708: L62-361* x Harosoy 63	Rps_1
OX900: Blackhawk x Harosoy 63	Rps_1
Indiana lines (supplied by Dr. K. L. Athow)	
PRX5-206 (Harosoy x PI 84,637)	$Rps_1{}^b$
PRX8-5 (Harosoy x PI 86,972-1)	Rps_3
Other	
PI 86,050 (Athow et al., 1980)	$Rps_1{}^c$, Rps_4
Sanga	$Rps_1{}^b$

*Dt_2 selection from Harosoy^6 x T117.

Table 3

F_2 segregations for an expected 3:1 ratio involving the L62-904 gene

Cross	Race	Resistant		Susceptible		Chi-square	P
		O	E	O	E		
L62-904 x OX708	3	38	43.5	20	14.5	2.30	0.20-0.10
L62-904 x OX900	3	40	43.5	18	14.5	0.83	0.40-0.30

O = Observed E = Expected

Table 4

F_2 segregations for an expected 9:3:3:1 ratio involving Rps_1^b and the L62-904 gene

Cross	Reaction to races 2 and 6-7				Chi-square	P
	RR	RS	SR	SS		
L62-904 x Sanga						
Observed	59	27	21	10		
Expected	71.4	23.8	23.8	7.9	3.47	0.50-0.30
L62-904 x PRX5-206*						
Observed	66	18	13	10		
Expected	60.1	20.1	20.1	6.7	4.75	0.20-0.10

*PRX5-206 is (Harosoy x PI 84,637).

Table 5

F_2 segregations for an expected 15:1 ratio involving the L62-904 gene and various other genes

Cross	Race	Resistant O	Resistant E	Susceptible O	Susceptible E	Chi-square	P
Rps$_1$							
L62-904 x OX708 + OX900	1	107	108.8	9	7.2	0.25	0.60-0.50
Rps$_3$							
L62-904 x PRX8-5	4	56	55.3	3	3.7	0.12	0.80-0.70
Rps$_4$							
L62-904 x PI86,050*	4	64	67.5	8	4.5	2.13	0.20-0.10
Altona - Rps							
L62-904 x OX693	4	105	103.1	5	6.9	0.30	0.60-0.50
Kingwa - Rps							
L62-904 x OX696	3,4,5	54	54.4	4	3.6	0.05	0.90-0.80

*F_2 seedlings inoculated as described by Ward et al. (1979); other crosses were F_3 seedling tests of F_2 plants using hypocotyl wounding/mycelium insertion (Buzzell et al., 1977).

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1) An allelism study of the inheritance of the lack of soybean lectin in five soybean lines.

Pull et al. (1978) found five soybean lines ('Columbia', 'Norredo', 'Sooty', T102 and 'Wilson-5') lacking the 120,000 dalton seed lectin, also called soybean lectin (SBL). Orf et al. (1978) established that the lack of SBL is inherited as a simple recessive, *le le*. The homozygous dominant

(*Le Le*) and heterozygous (*Le le*) condition result in the presence of SBL. In the above inheritance study only one of the five lines, T102, was used to determine the inheritance of SBL. The study reported herein was conducted to determine whether *le le* is allelic in the five lines lacking SBL.

A diallele set of crosses was made among the five lines Columbia, Norredo, Sooty, T102 and Wilson-5. Seeds were checked for the presence of SBL using the Ouchterlony (1948) double diffusion technique with SBL antiserum (Orf, 1979). Only a small chip of each seed is necessary for this nondestructive method. F_2 seeds were harvested from F_1 plants and 20 seeds from each cross were checked for SBL by the Ouchterlony method. No F_2 seeds were available for the cross T102 x Columbia.

All F_1 and F_2 seeds lacked SBL. The results indicate that *le le* is allelic in the five lines lacking SBL.

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2) Soybean seed β-amylase variants

Hildebrand and Hymowitz (1980a) reported that two soybean genotypes were found that lack detectable seed β-amylase activity. The cultivar 'Chestnut' produces an inactive β-amylase protein, Sp^{an} (Hildebrand and Hymowitz, 1980b); 'Altona' is a mixture of genotypes that have a β-amylase protein of normal activity ($Sp_1{}^{b}$) or lack it entirely (sp_1) (Hildebrand and Hymowitz, 1980b).

Chestnut was selected from 'Habaro' and introduced into the U.S. as PI 20,405 in 1906 from Kharbarovsk, USSR (Hymowitz et al., 1977). All 30 seeds of Habaro we tested for β-amylase were found to have normal β-amylase activity.

Moreover, there are vast differences between seed characteristics, plant growth habit, plant morphology, maturity, etc. between Chestnut and Habaro. Most likely Chestnut was selected from alien genetic material in the Habaro seed lot (R.L. Bernard, personal communication). Therefore, the origin of Chestnut apparently is unknown.

Altona was selected from the cross PI 194,654 x 'Flambeau' (Hymowitz et al., 1977). Flambeau was introduced into the U.S. in 1934 from the USSR (Hymowitz et al., 1977) and PI 194,654 was introduced into the U.S. from Sweden (Bernard, 1965). To determine if either of the parents of Altona was the source of the sp_1 alleles, 10 seeds of both Flambeau and PI 194,654 were tested for β-amylase activity. All seeds of both lines had normal β-amylase activity.

Altona was composited in the F_5 and it traces back to a single F_4 plant (Bernard and Lindahl, 1970). The most likely explanation for the situation in Altona is that a mutation occurred at the β-amylase locus in a F_4 seed on a F_3 plant, resulting in a heterozygous F_4 plant ($Sp_1^{\ b}\ sp_1$) genotype. Since both Altona genotypes probably trace back to a single F_4 plant, they represent near isogenic lines with about 94% of the loci having identical alleles. This is consistent with the lack of any differences in morphology or yield of these two genotypes in observation nurseries in Minnesota (J. W. Lambert, personal communication).

The lack of β-amylase activity in certain genotypes of Altona perhaps is due to amylase inhibitors (Jaffe and Lette, 1968). However, we found that mixing equal volumes of pH 5.0 acetate extracts of Altona ($Sp_1^{\ b}$) with extracts from Altona (sp_1) and incubating the mixtures at 4C for 24 hours gave an intermediate level of β-amylase activity. Also, the fact that sp_1 is recessive to $Sp_1^{\ b}$ indicates that sp_1 probably is due to mutation resulting in the lack of synthesis of the β-amylase protein (Hildebrand and Hymowitz, 1980b).

We have found no marked differences in chemical composition or carbohydrate metabolism in developing or germinating seeds of the soybean cultivars 'Williams' ($Sp_1^{\ b}$), Chestnut ($Sp_1^{\ an}$), Altona ($Sp_1^{\ b}$) and Altona (sp_1) (Hildebrand and Hymowitz, n.d.). Perhaps β-amylase in soybeans is just a storage protein or has some survival value such as conferring a greater level of resistance to a specific pest or pathogen.

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1) Effect of grafting date and maturity of the stock on the flowering behavior of soybean scions.

Many crosses made by midwestern U.S. soybean breeders are made between adapted genotypes and genotypes of later maturity. Due to a short growing season, soybean breeders in the northern U.S. are often unable to sufficiently delay planting of adapted genotypes to synchronize flowering with genotypes of later maturity. Photoperiod chambers are expensive and covering plants is time consuming and often produces cleistogamous flowers. Kiihl et al. (1977) demonstrated that grafting soybeans could be used as a tool to facilitate wide crosses.

This research was designed to examine the effect of grafting date and maturity of the stock on the flowering behavior of scions ranging in maturity from Maturity Group V to Maturity Group IX. It was hoped that this research might provide information which would enable soybean breeders to be more successful in using grafting for making wide crosses.

Materials and methods: Experiments were conducted at the Agronomy South Farm at Urbana, IL, during 1977 and 1978. At three different dates during the growing season, scions of 'Essex' (Maturity Group V), 'Ransom' (Maturity Group VII), 'Improved Pelican' (Maturity Group IX), and 'Jupiter' (Maturity Group IX) were grafted onto 'Hodgson' (Maturity Group I) and 'Williams' (Maturity Group III) stocks. Cultivars used as scions were grafted onto themselves (self-grafts) and left undisturbed (non-grafts) to serve as standards. Grafting dates were 7 July, 17 July, and 28 July in 1977 and 30 June, 11 July, and 20 July in 1978. A split-plot arrangement of a randomized complete block design with six replications was used. Grafting dates were considered the whole plots and the grafting treatments were considered the sub-plots. Days to first bloom were recorded.

The unbalanced nature of the data resulting from unsuccessful grafts prevented the valid comparison of the effect of years and scions in a split-plot analysis. As a result, a separate analysis of variance was conducted for each grafting date and year combination.

A modification of the "straw band" technique described by Bezdicek et al. (1972) was used for grafting. The stock was cut immediately above the

last fully expanded leaf. A wedge was made in the scion on the internode above the last fully expanded leaf. All partially expanded leaves were removed from the scion in order to reduce the risk of dessication. In addition, the grafts were made in the late afternoon such that the scion was initially exposed to a period of low-water demand. This eliminated the need for a plastic bag cover over the scion and graft.

Results and discussion: Although 63% of all scions produced flowers, a maximum of 92% of the Essex scions from the 4 July average grafting date produced at least one flower. The percentage of scions producing flowers decreased as the grafting date was delayed. In fact, only 35% of the scions grafted on the Hodgson stocks on the 24 July average grafting date produced flowers. Mean days from grafting to flower initiation decreased as the grafting date was delayed (Table 1). However, the decrease was generally insufficient to compensate for the delay in grafting. As a result, mean days from 1 July to flower initiation increased as the grafting date was delayed (Table 2). The genotype of the stock had a significant effect on the mean days from grafting to flower initiation (Table 1). The absence of significant stock x scion interactions in the analyses of variance indicated that the stock effects were consistent for the scions used in the experiment. Flowers were produced in the fewest number of days on scions grafted on the Hodgson stock on the 4 July average grafting date (Table 1). However, as the grafting date was delayed, scions on the Williams stocks tended to produce flowers in fewer days than scions on the Hodgson stocks (Table 1).

With the exception of the Essex and Ransom scions on the 24 July average grafting date, scions grafted on stocks of earlier maturity produced flowers earlier in the growing season than their non-grafted counterparts (Table 2). In the case of Improved Pelican and Jupiter, non-grafted plants did not initiate flowering before termination of the experiment on 1 September. On the other hand, the Essex and Ransom self-grafts initiated flowering an average of five days after their non-grafted counterparts (Table 2). Improved Pelican and Jupiter scions from the 14 and 24 July grafting dates produced flowers too late in the growing season (after 15 August) to be used for crossing purposes under Illinois conditions.

Summary: Grafting late maturity scions on stocks of earlier maturity appears to be a simple and effective means of hastening flowering of soybeans

grown in the northern U.S. Grafts should be made as early in the growing season as possible (before or near 1 July in central Illinois) on stocks of very early maturity (Group 0 or I) in order to obtain flowers on scions during a period when they can be used for crossing purposes. Under central Illinois conditions, scions as late as Maturity Group IX can be induced to flower by the first week of August.

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Table 1

Mean days from grafting to flower initiation

when averaged over two years

Average grafting date	Scion	Stock	
		Hodgson	Williams
		days	
4 July	Essex	26	28
	Ransom	29	33
	Imp. Pelican	34[a]	41
	Jupiter	33	37
14 July	Essex	21	24
	Ransom	28	30
	Imp. Pelican	36	37
	Jupiter	37	37
24 July	Essex	18	18
	Ransom	24	23
	Imp. Pelican	39	32
	Jupiter	40[a]	35

[a]Mean based on one year of data.

Table 2

Mean days from 1 July to flower initiation when averaged over two years

Scion	Stock	Not grafted	Average grafting date		
			4 July	14 July	24 July
		days			
Essex		36.0			
Essex	Essex		40	42	41
Essex	Hodgson		29	34	41
Essex	Williams		31	37	41
Ransom		47.5			
Ransom	Ransom		40+[a]	53	54+[a]
Ransom	Hodgson		32	41	47
Ransom	Williams		36	43	46
Imp. Pelican		*			
Imp. Pelican	Imp. Pelican		*	*	*
Imp. Pelican	Hodgson		37	49	62
Imp. Pelican	Williams		44	50	55
Jupiter		*			
Jupiter	Jupiter		*	*	*
Jupiter	Hodgson		36	50	63
Jupiter	Williams		40	50	58

*Did not produce flowers before termination of the experiment on 1 September.

[a]Means based on one year of data.

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2) An allele at the *rps*$_1$ locus from the variety 'Kingwa'.

Four genes at the same locus affecting reaction to phytophthora root rot have been previously identified.

Allele	Source	References
rps$_1$	Harosoy	Bernard et al. 1957 (as *ps*)
Rps$_1$	Mukden	" " " " (as *Ps*)
Rps$_1$[b]	PC 31745	Hartwig et al. 1968 (as *rps*^{2})
Rps$_1$[c]	Arksoy, PI 54615-1	Mueller et al. 1978

As part of our breeding effort to create adapted varieties with resistance from diverse sources we selected the variety 'Kingwa' which had been reported by Athow et al. (1974) to be resistant to several races of the phytophthora-rot organism. We used it as a donor parent in backcrossing programs with the varieties 'Clark' (Group IV), 'Corsoy' (Group II), 'Wells' (Group II), and 'Williams' (Group III). During backcrossing the resistance appeared to be controlled by a single dominant gene which we tentatively designated *Rps*^{k}. Further evidence of this was obtained during selection and testing in generations after the final backcross and is presented below for Corsoy and Williams.

We hypocotyl-inoculated the progenies of 39 F_1 plants of Corsoy^{8} x Kingwa with mycelium of race 5 and found 19 to be all-susceptible and 20 to be segregating for resistance (expected = 19.5:19.5, probability of a larger chi-square P = 0.9). The 20 segregating families totalled 238 resistant F_2 plants and 87 susceptible ones (expected = 243.8:81.3, P = 0.5). Forty-two resistant F_2 plants were grown to maturity and progeny tested with race 5. Twenty-eight segregated and 14 were found to be true-breeding for resistance (expected = 28:14, P = 1.0).

Likewise, using race 5 with Williams^{7} x Kingwa we found that, of the progenies of 18 F_1 plants, there were 11 all-susceptible and 7 segregating (expected = 9:9, P = 0.3). The 7 segregating families totalled 59 healthy and 11 infected F_2 plants (expected 52.5:17.5, P = .07). Of 32 resistant F_2 plants grown to maturity 20 segregated and 12 produced all-resistant progenies (expected 21.3:10.7, P = 0.6).

We then tested resistant progenies from both the Corsoy and Williams backcrosses with other races and found them to be resistant to races 1 through 9. Additional testing here by C. D. Nickell (personal communication) has shown them to be resistant also to races 10, 13, 14, and 15, but to be susceptible to races 12 and 16 (race 11 not available).

We next attempted to combine *Rps*^{k} with other genes for resistance. We crossed a resistant Corsoy isoline from Corsoy^{8} x Kingwa (designated L27) with an isoline from Corsoy^{6} x Lee 68 with the *Rps*$_{1}^{c}$ gene, which was released commercially as 'Corsoy 79'. In testing of Corsoy 79 x L27 with race 5, to which Corsoy 79 is susceptible, we found 75 healthy and 30 infected F_2 plants (expected 78.8:26.2, P = 0.4). However, all 312 F_2 plants tested with race 1 were resistant. Since Corsoy 79 and L27 each have monogenic resistance to race 1 and no susceptible F_2 plants segregated, we concluded that *Rps*^{k} is at

the same locus as Rps_1 and should be designated Rps_1^k.

Similarly, we tested a Williams-Rps_1^k isoline from Williams[7] x Kingwa, designated L24, by crossing with an Rps_1^c isoline from Williams[6] x Lee 68 released as 'Williams 79'. In tests of Williams 79 x L24 with race 5, to which Williams 79 is susceptible, there were 256 healthy and 89 infected F_2 plants (expected 258.8:86.2, P = 0.7). All 165 F_2 plants tested with race 3 were resistant.

We also crossed L24 with L26, an isoline from Williams[7] x Harrel, with another allele at locus 1 Rps_1^b. L26 is susceptible to race 2 but resistant to 1 and 3 through 9. When tested with race 2 there were 67 healthy and 30 infected F_2 plants (expected 72.8:24.2, P = 0.18), but all 114 F_2 plants tested with race 1 and all 108 tested with race 5 were resistant. This agrees with the evidence from the Corsoy isolines that the gene from Kingwa is at the rps_1 locus.

Since the only difference between Rps_1^b and Rps_1^k appears to be its reaction to race 2 we again inoculated the Williams isolines and again found Rps_1^b to cause a susceptible and Rps_1^k a resistant response to this race.

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1) Evidence of a major gene controlling the resistance to race 5 of *Cercospora sojina*.

Phillips and Boerma (1981) identified race 5 of *Cercospora sojina* Hara causing frogeye leafspot, in 1978. Many commonly grown soybean cultivars were found to be susceptible to race 5. A study was initiated in 1979 to determine the inheritance of resistance to race 5. Crosses between resistant and susceptible cultivars were made in the greenhouse, using the resistant cultivars 'Lincoln' and 'Davis' and the susceptible cultivars 'Blackhawk' and 'Hood'. The F_1 and F_2 plants were grown in the greenhouse and inoculated by atomizing (2.5 ml/plant) a conidial suspension (concentration - 6×10^4 spores/ml) onto the upper and lower leaf surfaces when the plants were at the two or three trifoliolate leaf stage. A high relative humidity was maintained after inoculation by placing F_1 plants in a moist chamber for 72 hr and placing a clear plastic bag over F_2 plants for 72 hr. Ratings were made 10 to 14 days after inoculation. Resistant plants showed no or only a few small lesions and susceptible plants showed numerous large spreading lesions.

The F_1 plants from crosses between resistant and susceptible cultivars were all resistant. The segregation of these crosses in the F_2 generation is shown in Table 1.

Table 1

Segregation of the reaction to race 5 of frogeye leafspot in the F_2 generation of four soybean crosses

Cross	No. of plants			3:1 chi-square probability
	Resistant	Susceptible	Total	
Blackhawk x Davis	152	52	204	0.8-0.9
Blackhawk x Lincoln	104	30	134	0.4-0.5
Davis x Hood	161	49	210	0.5-0.6
Lincoln x Hood	153	56	209	0.5-0.6
Total	570	187	757	0.8-0.9

The F_2 populations segregated as expected assuming monogenic control and complete dominance with resistant and susceptible plants occurring in a 3:1 ratio. All chi-square values for tests of goodness of fit, within individual crosses and pooled over crosses were acceptable. The agreement of the classification of the crosses Blackhawk x Davis and Davis x Hood, where Davis (resistant parent) was either the maternal or paternal parent, indicated there was no cytoplasmic or maternal effect on the expression of resistance.

Athow and Probst (1952) and Probst et al. (1965) have reported the resistance to races 1 and 2 is conditioned by the genes Rcs_1 and Rcs_2. The inheritance of resistance to races 3 and 4 is unknown. It appears the resistance to race 5 is conditioned by a third major gene. We are in the process of screening the F_3 generation of the crosses in Table 1. Since Hood is resistant to race 2 and susceptible to race 5 and Lincoln has the opposite reaction to these two races, F_3 lines from this cross are also being inoculated with both races to determine the relationship between the two genes for resistance. Since cultures of races 1, 3, and 4 have not been obtained, the relationship of the genes for resistance to these races to the gene for resistance to race 5 cannot be determined.

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1) Breeding soybean for drought tolerance.

The extension of soybean cultivation in the south part of Europe is limited by climatic conditions and, above all, by drought appearing each year during summer, in a time which is a critical period for water supply of soybeans: the grain and pod filling stages (Mingeau, 1975). By action of this drought, grain yields may decrease drastically. As irrigation is often impossible, one of the most important breeding objectives in France is drought tolerance. Although water relations often should be studied in soybeans, varietal differences were rarely investigated except by Mederski and Jeffers (1973) and Sammons et al. (1978, 1979).

In order to search for simple, easy to measure parameters, 15 indeterminate varieties coming from several countries (Table 1) were cultivated in drought boxes (1 m^2 x 0.6 m depth) and kept, from flowering time until maturity, under two water supply levels:

- treatment A: Severe drought stress
- treatment B: No drought

Every two weeks, plants were harvested in each variety and each treatment and canopy parameters were measured. At maturity time, seed yield and its components were determined.

To estimate the drought-tolerance level of the tested varieties, the following index, based on seed production, was used:

$$\text{Drought Tolerance Index (DTI)} = \frac{\text{Seed dry weight in treatment A}}{\text{Seed dry weight in treatment B}} \times 100$$

The value of DTI for each variety is presented in Table 1. A genetic variability appears for drought tolerance and allows us to think that a breeding program for that character could be successful.

In order to search for parameters well correlated with DTI, a stepwise regression analysis was done between DTI and the canopy parameters measured on plants in treatment A. The following equation was achieved:

Table 1

Drought Tolerance Index (DTI)

Cultivar	Maturity group	Origin	D T I
Kagon	I	U.S.A.	57.7
Giessen 456-64	0	Germany	56.1
Amsoy 71	II	U.S.A.	53.8
F 68-199	0	Romania	52.1
Kirovograska	I	USSR	51.7
Wolfsthaler	I	Germany	51.3
Harman	II	U.S.A.	48.6
IASI 10	II	Romania	45.9
Szurkebarat	0	Hungary	44.3
SRF 100	I	U.S.A.	43.2
Wysokonoska	00	Poland	41.3
Grant	0	U.S.A.	40.9
Nepolegajuskaia II	III	USSR	40.2
Hodgson	I	U.S.A.	39.6
A-100	II	U.S.A.	39.2

(a) DTI = 0.35 SLWD + 15.88 SPW - 0.67 SLW + 1.81 MPL - 3.82 PWC + 3.01 LWC + 124.6

with: SLWD: Specific Leaf Weight Decrease between "R_5" and "R_5+15 days" stages

SPW: Specific Petiole Weight next from R_3 stage

SLW: Specific Leaf Weight next from R_3 stage

MPL: Mean Petiole Length next from R_3 stage

PWC: Petiole Water Content next from R_3 stage

LWC: Leaf Water Content next from R_3 stage.

With these six variables, the multiple regression coefficient is R = +0.96. So that 92% of the total DTI variation is taken into account by equation (a).

Therefore, drought-tolerant varieties seem to be mainly characterized by:

- a fast SLWD during pod filling
- a rather high SPW around R_3 stage
- a rather low SLW around R_3 stage.

The entrance of these variables in the equation seems to indicate that the assimilates transport from leaves to seeds plays an important part in drought tolerance.

Another regression analysis was done between DTI and the canopy and yield parameters measured on plants in treatment B (without drought). The following equation was achieved with six first variables.

(b) DTI = 1.79 PWC + 26.03 SPW + 3.47 LWC + 0.21 SLWD - 0.19 MLS - 0.08 SPWD - 30.1

with same symbols as before, and:

MLS = Mean Leaf Surface next from R_3 stage

SPWD = Specific Petiole Weight Decrease between "R_5" and "R_5+15 days" stages.

With these six first steps, the multiple regression coefficient is R = +0.89. Therefore, 79% of the total DTI variation is taken into account by equation (b). But the study of the residuals shows that their value is not independent of DTI. So, it seems difficult to estimate the DTI by measurements made on non-stressed plants.

Nevertheless, it is interesting to observe that the seed yield parameters did not enter first the regression equation but the canopy parameters and, also, that it is rather the same variables which compose the two equations (a) and (b):

- Specific Leaf or Petiole Weights and their decrease before maturity
- water contents of canopy parts
- Mean Leaf Surface or Mean Petiole Length which are variables related to cell enlargement.

Moreover, the signs of these variables are nearly the same in the two equations (unless for MLS and MPL): that means that drought tolerance is not the result of a drastic modification of structures of the plant but the result of an adaptation of these structures to drought conditions.

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1) Comparison of subunit compositions and isolectin profiles of the seed lectins purified from *Glycine max* and *G. soja*.

The presence of the 120,000 dalton soybean seed lectin (SBL) is controlled by a simple dominant gene designated *Le* (Orf et al., 1978). A recent immunological survey of the USDA soybean [*Glycine max* (L.) Merr.] collection indicated that 2,646 of 2,664 lines are *Le* (Stahlhut and Hymowitz, 1980), and an analogous study of the USDA *G. soja* Sieb. & Zucc. collection indicated that 285 of 559 lines contain SBL (Stahlhut et al., 1981). SBL preparations from seeds of the soybean lines 'Beeson', D68-127, 'Disoy', 'Forrest', 'Harosoy 63', and T-247 apparently are identical; electrophoresis under denaturing conditions separated each lectin into two types of subunits, and isoelectric focusing resolved each into a complex mixture of isolectins (Su et al., 1980). Here I report the results of an analysis of the seed lectins from 93 additional *G. max* lines and from one *G. soja* line. The objectives were (i) to determine if there is variation in subunits or in isolectins of SBL isolated from a representative sample of *G. max* genotypes and (ii) to provide initial biochemical characterization of the *G. soja* seed lectin.

Seeds were kindly provided by Dr. Theodore Hymowitz, University of Illinois, and by Dr. Kuell Hinson, University of Florida. SBL from defatted seed meals was purified to homogeneity by affinity chromatography as described previously (Bhuvaneswari et al., 1977). Polyacrylamide disc gel electrophoresis in the presence of sodium dodecyl sulfate was according to Laemmli

(1970). The polyacrylamide concentration in the separating gels was 10%, and 10 µg samples of the lectin (which had been boiled in the presence of 2-mercaptoethanol) were electrophoresed in 8 x 0.5 cm cylindrical gels at 3 mamp/gel. Protein was stained with Coomassie Brilliant Blue R-250. Lectin samples (40 µg) were isoelectric focused in 5.5 x 0.5 cm gels containing 5% acrylamide and 2% Bio-Lyte 3/10 ampholytes (from Bio-Rad). Focusing was done according to the directions of the ampholyte manufacturer, and gels were stained with Coomassie Brilliant Blue R-250.

There was no observed variation in the subunit composition or in the isolectin profiles of SBL from seeds of the following soybean lines: Ada, Adelphia, A.K. (Harrow), Amsoy, Anoka, Aoda, Bansei (Ames), Bavender Special B, Bombay, Capital, Cayuga, Chippewa, Chusei, Clay, Cloud, Corsoy, Cutler 71, Dunn, Early White Eyebrow, Ennis I, Fabulin, Fiskeby V, Flambeau, Fuji, Funk Delicious, Giant Green, Gibson, Granger, Green and Black, Harbinsoy, Harcor, Hardee, Harman, Harwood, Higan, Hokkaido, Hoosier, Illini, Imperial, Jogun, Jupiter, Kabott, Kagon, Kent, Kim, Kura, Linman 533, Little Wonder, Madison, Magna, Manchu (Lafayette)B, Manchuria 13177, Mandarin, Manitoba Brown, Medium Green, Merit, Mingo, Mokapu Summer, Morse, Norma, Ogemaw, Oksoy, Ontario, Ottawa, Peking, Perry, Portage, Portugal, Protana, Provar, Rampage, Ross, Sato-3, Scott, Seedmakers, Sioux, Soysota, SRF 400, Steele, Swift, Tortoise Egg, Vansoy, Viking, Waseda, Wea, Wilson, Wilson 5B, Wilson 6, Wing Jet, Wisconsin Black, Wolverine, Wye, Yellow Marvel. The results were unexpected because heterogeneity in legume seed lectins often is pronounced and may be under genetic control (Murphy and Goldstein, 1979; Pueppke, 1979). Soybean seeds, however, are apparently of just two types: those that contain a complex mixture of SBL isolectins and those that lack SBL entirely.

Seeds of *G. soja* 339,731 contained a lectin that was identical to *G. max* SBL by the above biochemical criteria. The lectin comprised 1.1% of the protein solubilized from seeds of 339,731 (compared to 1.2% for SBL from both 'Hardee' and 'Jupiter', which were extracted at the same time). Although detailed biochemical screening of *G. soja* lectins is unfinished business, the results presented here indicate that the SBL molecule is structurally conserved in and may be characteristically produced by both *G. soja* and *G. max*.

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1) Potential of exotic soybeans in the sub-montane region of Himachal Pradesh (India).

Himachal Pradesh is a hilly state of Northern India, with its global location between $75^{\circ}45'$ - $79^{\circ}04'$ E longitude and $30^{\circ}22'$ - $33^{\circ}12'$ N latitude. In this part of the country, soybean is indigenously grown as a rainy season crop up to an altitude of 1800 m above mean sea level. The indigenous soybean comprise small seeded, twining type low-yielding varieties. An improved variety with medium seed size, profuse branching and prolific bearing had been tested and released for cultivation in this part of the country long before the initiation of the All India Coordinated Project on soybean. With the

advent of the said project several exotic varieties were tested and recommended for cultivation in different zones of India. Varieties 'Clark' and 'Lee' were recommended for cultivation in the Northern Hill Zone of India. 'Bragg', recommended for cultivation in the Northern Plain Zone, adjoining Himachal Pradesh, due to its popularity as a high yielding variety, found its way in the sub-montane region of the state and gradually spread to the mid-hill zone also.

However, soon after the introduction of Bragg, the problems of defective germination, poor stand and wide fluctuations in yield were frequently encountered by the cultivators. It was, therefore, felt necessary to identify a variety of soybean, out of the available indigenous and exotic stocks, suitable for cultivation in the sub-montane region of the state. Thirty-two soybean varieties were tested at Kangra (700 m above mean sea level) during 1970. Out of these, the top five varieties, namely, 'Jackson', 'Hardee', 'Bienville', 'Hampton' and 'Pickett', were selected for further testing.

This set of five varieties was evaluated for grain yield for a number of years at Kangra along with Bragg and 'Punjab No. 1'. The yield data for the period 1971-1977 are given in Table 1, along with mean number of days taken to mature.

A perusal of the data in the table indicates that the performance of Bragg was not statistically superior to Punjab No. 1 during any of the years. In 1971 and 1977, none of the varieties exceeded Punjab No. 1 by a significant margin. On the other hand, Pickett gave significantly poorer performance than Punjab No. 1 during both these years. In 1972, all new varieites except Jackson surpassed Punjab No. 1 by a significant margin, while in 1973, the performance of all the five varieties was significantly superior to Punjab No. 1. In 1974, one; in 1975, three; and in 1976, two of the varieties outyielded Punjab No. 1 significantly.

Variety Jackson gave the highest yield of 3796 Kg/ha during 1976. However, its mean performance over years was only 6% superior to Punjab No. 1, while it was 5 days later in maturity than the latter. Varieties Bienville and Hampton, having a mean maturity period of about 130 days, outyielded Punjab No. 1 by about 16%. With this mean performance, these varieties appear more promising than Bragg for introduction in the region.

Variety Hardee gave the highest mean performance of 3144 Kg/ha, which was 32.82% superior to Punjab No. 1, which the former beat by a significant

Table 1

Yield performance of exotic soybean varieties tested at Kangra during the period 1971-77

Variety	Yield Kg/ha								Percent increase over Punjab No.1	Mean No. of days to maturity	Yield (Kg) per day per ha.
	1971	1972	1973	1974	1975	1976	1977	Mean			
Hardee	2283	3549*	3185*	3291*	3254*	3333	3111	3144	32.82	136.6	23.03
Bienville	1914	3301*	3000*	2972	2581*	2994	2429	2742	15.84	130.3	21.04
Hampton	1821	3116*	2704*	2583	3059*	3643*	2311	2748	15.92	129.3	21.25
Jackson	1925	1901	2778*	2569	2301	3796*	2400	2524	6.63	125.6	20.01
Pickett	1574	3024*	2630*	2048	2133	2778	2029	2317	-2.12	123.0	18.23
Bragg	1790	---	2417	2301	2146	3209	2489	2392	1.05	126.5	18.90
Punjab No. 1	2098	1944	2130	2430	2217	3024	2726	2367	---	120.5	19.64
Mean	1915	2806	2692	2596	2527	3254	2498	2605			
C.D. @ 5%	518	561	462	591	314	490	540				

*Significantly better than Punjab No. 1.

margin four times in a row (1972-1975). Hardee scored as the highest yielder in all the years except 1976, which incidentally was the best year, and the performance of Hardee (3333 Kg/ha) was quite close to the mean performance (3254 Kg/ha). During rest of the six years its performance was far superior to the mean performance of varieties. In spite of Hardee's late maturity of 137 days, its per-day-per-hectare productivity was the highest (23 Kg).

It is of interest to note that variety Hardee did not give only high average yield but also exhibited average stability over the years. It was found to possess resistance to diseases like bacterial leaf pustule, frog-eye-spot and bud blight, under field conditions.

The only demerit of the variety is its late maturity, which, looking at its productive potential, merits a sacrifice. However, the growers in the region would remain contented with average yielding varieties like Punjab 1 and Bragg because of their comparative earlier maturity, so long as soybean remains a non-remunerative crop due to its poor marketability.

It is felt that whenever soybean attains the status it deserves in India, one could bank upon the merits of Hardee for achieving high production levels and getting maximum returns. However, the variety has not been relegated to obscurity and is being used in our hybridization programs to exploit its high yield potential.

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2) Study on biological measures of environment and its implications on the physical limits to seed yield and other developmental traits in soybean.

Since adaptation of soybean and its dependence on various geographical and climatological factors has been a subject of debate (Byth, 1976; Summerfield and Minchin, 1976; Whigham, 1976), therefore, in the present study an attempt has been made to measure the environment biologically and to discuss the same in the light of physical limits of environment.

Materials and methods: The experimental material consisted of 40 entries, representing 36 F_4-derived lines of an inter-varietal cross, two parents involved in this cross, Pb 1 and D60-9647, and two standard varieties, 'Lee' and 'D.S. 73-8'. The F_4-derived lines were selected out of the 74 progenies,

raised and evaluated during Kharif, 1977, for seed yield, specific gravity, and hundred-seed weight. These selected lines represented all categories (low, medium and high) of seed size and specific gravity. These 36 F_4-derived progenies were designated genotypes 1 to 36. Soybean Pb. 1, D60-9647, Lee and D.S. 73-8 were designated genotypes 37, 38, 39, 40, respectively.

These 40 entries were raised in a randomized complete block design with two replications, at the experimental farms of the Department of Plant Breeding and Genetics, at Palampur (1290 m above mean sea level), Kangra (700 m above mean sea level), Katrain (1500 m above mean sea level), and Khaltoo-Solan (1320 m above mean sea level). At Palampur, the same set of material also was raised in association with maize as intercrop (one row of soybean, between two rows of maize, 75 cm apart) in randomized complete block design with two replications. Each entry in monoculture was grown in a single 2 m row in each replication. Row-to-row distance was 45 cm and plant-to-plant, 4 cm. Recommended dose of fertilizer was applied at the time of sowing.

Entries were evaluated for seed yield and its components, seed quality traits, structural components and physiological traits. The technique suggested by Finlay and Wilkinson (1963) was used to measure the environment biologically. The measure, which was obtained as the mean of all the entries at j^{th} environment minus the grand mean, was designated as environmental index, with respect to j^{th} environment.

Results: With respect to different groups of traits, results obtained on the estimates of environmental index (Table 3), for measuring the environments, are presented below.

For seed yield and its components, Solan and Katrain locations were the best for the expression of genetic potential. For seed yield per plant and pod length, Katrain was the best, while for pods per plant and pods per main stem, Solan was the best. Kangra had a poor environment for almost all the components except pods per plant and seeds per pod. Palampur-intercropping, as well as monoculture, were poor environments for all the components except seeds per pod for which latter environment (Palampur-monoculture) was the second best.

For seed quality traits, no definite pattern could be established. The best environment for percent laboratory germination was Solan, followed by Palampur-monoculture, while Kangra and Katrain were the average environments. For percent field emergence, Katrain was the best, while Solan, Palampur-monoculture and Kangra were the average environments. Palampur-intercropping was

the poorest environment for these two traits. For low percentage of hard seeds, Solan represented the best followed by Palampur-monoculture and Katrain, while Kangra was the best for high percentage of hard seeds. For hundred-seed weight and hundred-seed volume, favorable environments were Solan, Palampur-monoculture as well as intercropping. For seed density, Katrain was the only favorable environment. For high seed specific gravity index, Kangra followed by Palampur-intercropping, were good environments, while Palampur-monoculture followed by Solan and Katrain favored low seed specific gravity index.

Regarding structural components, Solan environment was the best for petiole length and internode length, good for plant height, average for primary branches per plant and poor for nodes per main stem. Palampur-monoculture was the best environment for plant height, good for primary branches per plant and nodes per main stem, but poor for internode length. Katrain environment was good for plant height, average for nodes per main stem, but poor for primary branches per plant and petiole length. Kangra environment proved to be the best for primary branches per plant and nodes per main stem, average for internode length, but poor for plant height. Palampur-intercropping was the poorest environment for all the traits except plant height for which it was average.

Early flowering was induced in Solan and Kangra, while reverse was true for Palampur-monoculture. For early maturity, Katrain was the best, followed by Palampur-intercropping, while Palampur-monoculture, Solan and Kangra favored late maturity.

For pod potential per node, the only good environment was Solan, all others being unfavorable. For leaf potential per plant, the environment at Katrain proved to be the best and that at Solan the worst, but the trend for leaf area was just the reverse.

Discussion: Breese (1969) has pointed out that joint measures of environments of the genotypes can provide a basis for better understanding of physical limits of environments. Therefore, the implications of the results obtained on environmental index (Table 3) in the present study might provide a stimulus for the analysis of environmental limitations for higher yields in soybeans.

It will be interesting to examine geographical and climatic conditions at Palampur, Solan, Katrain and Kangra, with particular reference to their bearing on seed yield, germinability, seed density and seed specific gravity index.

Table 1

Geographical situation of different locations

Geographical parameters		Locations			
		Palampur	Khaltoo-Solan	Katrain	Kangra
1	Altitude (meters)	1290	1320	1500	700
2	Latitude	32°6'	30°1'	32°5'	30°5'
3	Longitude (east)	76°3'	77°1'	77°9'	76°2'

Table 2

Monthly meteorological data for Kharif 1978

at different environments

Months	Location	Temperature (°C)		Rainfall (mm)
		Max.	Min.	
June	Palampur	28.9	21.1	465.6
	Solan	31.8	17.3	326.2
	Katrain	28.3	17.6	90.6
	Kangra	-- [a]	--	--
July	Palampur	25.0	19.6	1072.8
	Solan	27.9	17.5	245.8
	Katrain	26.5	18.4	195.0
	Kangra	--	--	--
August	Palampur	25.2	19.6	929.9
	Solan	29.0	16.6	326.2
	Katrain	25.6	18.6	194.0
	Kangra	--	--	892.9
September	Palampur	25.7	17.0	310.7
	Solan	27.6	14.4	245.8
	Katrain	24.4	13.8	106.8
	Kangra	--	--	166.3
October	Palampur	24.3	13.9	5.8
	Solan	28.2	9.2	0.0
	Katrain	23.5	9.0	10.0
	Kangra	--	--	0.0
November	Palampur	19.1	9.5	53.3
	Solan	--	--	19.0
	Katrain	16.0	3.4	166.5
	Kangra	--	--	5.0

[a]Data not available.

Table 3

Estimates of environmental indices for different groups of characters

Characters	Environments I Palampur (mono-culture)	II Solan	III Katrain	IV Kangra	V Palampur (inter-cropping
A. Seed yield and its components					
1. Seed yield/ plant (gm)	-4.49*	8.25*	8.63*	-2.11*	-10.27*
2. Pods/plant	-9.15*	23.71*	1.84	8.81*	-25.22*
3. Pods/main stem	-3.84*	6.69*	2.26*	-0.91*	- 4.20*
4. Pod length (cm)	-0.23*	0.33*	0.76*	-0.26*	- 0.61*
5. Seeds/pod	0.20*	0.35*	--	0.01	- 0.56*
B. Seed quality traits					
1. Percent lab. germination	5.89*	6.76*	1.43	2.49	-16.57*
2. Percent field emergence	-0.80	2.25	9.94*	-4.16	- 7.24*
3. Percent hard seed	-1.20*	-1.70*	-1.04*	3.85*	0.08
4. Hundred seed weight (gm)	1.30*	2.59*	-2.45*	-1.87*	0.43*
5. Hundred seed volume (cc)	1.07*	2.20*	-2.18*	-1.52*	0.43*
6. Seed density (gm/cc)	-0.0004	-0.0038*	0.0153*	-0.0046*	- 0.0064*
7. Seed specific gravity index (floating percentage)	-15.49*	-8.09*	-4.10*	16.03*	11.65*
C. Structural components					
1. Plant height (cm)	4.06*	3.31*	2.20*	-9.99*	0.42
2. Primary branches/ plant	0.73*	0.62*	-0.45*	1.80*	-2.70*

Table 3 - *continued*

Characters	Environments				
	I Palampur (mono-culture)	II Solan	III Katrain	IV Kangra	V Palampur (inter-cropping
3. First internode length (cm)	-0.42*	1.52*	--	0.03	-1.14*
4. Petiole length (cm)	--	8.47*	-1.20*	--	-7.28*
5. Nodes/main stem	1.93*	-0.68*	0.12	2.31*	-3.68*
D. Phenological traits					
1. Days to first flowering	8.63*	-6.25*	--	-2.38*	--
2. Days to maturity	10.77*	5.50*	-13.86*	2.85*	-5.26*
E. Physiological traits					
1. Pod potential/node	-0.59*	1.42*	--	-0.45*	-0.39*
2. Leaf potential/ plant	--	-19.56*	19.56*	--	--
3. Leaf area/plant	--	5.56*	-5.56*	--	--

*Significant at 5% level from zero.

Geographical factors: Geographical situation (Table 1) appears to have marked effect on the above mentioned four economic seed traits and thus to influence soybean adaptation. Higher altitude, with temperate to sub-temperate climate, appears to be responsible for better adaptation, leading to favorable effects on seed yield, germinability and high seed density (Basnet et al., 1974; Singh, 1976; Byth, 1976; Delouche and Rodda, 1976). However, low yields at higher altitude have been reported by Whigham (1976) and Basnet et al. (1974). Sub-temperate climate at a high altitude might not be congenial for high expression of oil content as indicated by low seed specific gravity index at higher altitude as compared to low altitude climate.

Increase in percentage of hard seeds, marring the cooking quality of soybean, from higher to lower altitude, probably might be responsible for its

poor acceptability as a pulse in sub-tropical and tropical countries like India. However, it is worth mentioning that in the hilly region of India, at high altitudes, soybean is being used from the day of its introduction, like other pulses.

Climatic factors: Besides the effect of altitude on soybean adaptation, it will be worthwhile to look at the rainfall, day and night temperature during the growing season of the crop in relation to high yield and other economic seed traits (Table 2). It appears that distribution of rainfall at different locations during the growth period of soybean, specifically in reproductivity phase, might have been a major physical factor in determining the yield per plant in all the altitudes. The poor yield obtained at Palampur, in spite of being located at a higher altitude having sub-temperate climate, appears to be due mainly to very high rainfall creating waterlogging conditions in the field. The other factor involved may be the zinc deficiency in the acidic soil of Palampur, recently reported by Kanwar (1979). Sensitivity of soybean plant towards this micronutrient is well-known (Byth, 1976). In spite of being a good environment for more pods per plant, the lowest yields at Kangra might be due to uneven distribution of rainfall, creating stress conditions at critical stages of development. The duration of vegetative growth at Kangra was also longer as compared to that at Solan. The negative correlation of duration of vegetative growth with seed yield has been well documented (Summerfield, 1975; Byth, 1976). This fact is further supported by the high yield obtained at Solan where the duration of vegetative growth was shorter because of the locality providing the best environment for induction of early flowering.

The high yield at Solan and Katrain is also understandable in the light of recent investigation on the effect of night temperature in induction of flowering in soybean. The consistently comparatively lower night temperature at these locations, during the growing period of the crop induce early flowering and thereby reduce the duration of vegetative growth (Summerfield, 1975).

Besides other factors mentioned above, the lowest yield at Kangra apparently also followed from the high day temperature in the sub-tropical climate of the location during the cropping season (though data is not reported due to its non-availability). This contention gets support from the report of Summerfield (1975), who has observed that warmer ($33^{o}C$), as compared to

cooler (27°C), day temperature reduces the seed yield in soybean, by adversely affecting fertilization and pod setting. In view of this, high yield at Solan might be due to availability of optimum day temperature.

Conclusion: It can be concluded that very high rainfall, its uneven distribution during different phases of growth, high day and night temperature, besides altitude, might be the major yield-limiting factors in soybean. However, in recent years, the yields obtained from different genotypes in tropical to sub-tropical climate have been comparable to those in temperate climates, suggesting a cautious approach in the interpretation of the above conclusions drawn on physical limiting factors for high yield (Singh, 1976; Whigham, 1976; Shanmugasundaram, 1976).

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3) Influence of cropping system on seed yield, seed quality and other developmental traits and its implications on ideotype required in soybean for intercropping in maize.

Generally, in India and particularly in the hilly region of the country, due to small holdings, farmers usually follow intercropping system for an assured and stabilized production. This consideration becomes more important in the light of recent comments of Baker (1975) about the unacceptability of agricultural research on soybean with monoculture system, by the farmers in West Africa where intercropping is the general practice. This raises the question concerning development of ideotypes and their suitability for intercropping. In the present communication, an attempt has been made to understand the influence of intercropping system on the expression of various economic traits and different response of genotypes for tailoring an ideal plant type by growing 40 different genotypes of soybean in a randomized block design with two replications in monoculture as well as in association with maize at Himachal Pradesh Agricultural University, Palampur, which is situated 1200 m above mean sea level, during rainy season of 1977. Each entry in monoculture as well as in with maize as intercrop (one row of soybean between two rows of maize 75 cm apart) was grown in a single 2 m row in each replication. In monoculture, the row-to-row distance was 45 cm. Each entry was evaluated for different groups of characters as mentioned in Table 1.

Influence of cropping system: Analysis of variance indicated that significant differences existed among genotypes for different groups of traits studied. Estimates of mean for different groups of characters obtained over genotypes in monoculture and in intercropping with maize are given in Table 1. It can be seen from this table that the yield per plant in the intercropping micro-environment has been reduced to the extent of more than 80% as compared to monoculture. Except pods per main stem and pod length, all other yield components were drastically reduced (pods per plant and seeds per pod). Other

characters whose potential is being lowered in intercropping are percent laboratory germination, seed density, primary branches per plant, nodes per main stem and days to maturity. However, intercropping appears to be providing favorable micro-environment for the expression of high seed specific gravity index and in turn high oil content. Similarly, this environment also favors high frequency of hard seed. Reduction of soybean yield in intercropping as compared to monoculture has also been reported earlier (Pendleton et al., 1963; Buttery, 1970; Kumar, 1976; Kwon and Won, 1979). However, according to Triplett (1962), soybean yields are not reduced in maize-soybean intercropping system.

The report on the influence of intercropping on other traits is limited. The adverse effect of intercropping on seed yield, germinability and seed density can be explained if one considers the environment of the plant as a zone of the activity of various physical and chemical factors outside the plant, which may be modified by size, number and arrangement of constituents of plants. The canopy structure, radiation intensity, temperature, wind, and CO_2 concentration around the individual plant influence various processes involved in photosynthesis which in turn produces yield (Okibago, 1975). Reduction of photosynthetic activity due to shading has been well-documented by Johnston et al. (1969). Half net assimilation rate (NAR) value of soybean in comparison to maize might also be a major factor in reducing the soybean yields in intercropping system (Buttery, 1970). Not only the micro-environment above the soil around the plant is changed due to intercropping but root zone is also considerably affected. Wahua and Miller (1978) have shown that if soybean is intercropped with tall sorghum, due to shading and competition effects, nitrogen fixation by soybean is reduced to the extent of 99%, mainly due to reduction in number of nodules per plant, weight per nodule and specific nodule activity. Contrary to the present findings about the reduction in seed density (protein content) and increase in seed specific gravity index (oil content), Wahua and Miller (1978) have reported reduction in oil content but no effect on seed protein due to intercropping. This might be due to differential competition of soybean with sorghum and maize, but if one considers the results about reduction in nitrogen fixation in intercropping with sorghum, even the decrease in protein content, recorded in present study is more convincing.

Table 1

Estimates of means for different groups of characters in monoculture and intercropping with maize

Characters	Monoculture	Intercropping
A. Seed yield and its components		
1. Seed yield/plant (g)	6.91	1.13
2. Pods/plant	23.74	7.67
3. Pods/main stem	5.53	5.17
4. Pod length (cm)	3.76	3.39
5. Seeds/pod	2.32	1.55
B. Seed quality traits		
1. Percent laboratory germination	90.89	68.43
2. Percent field emergence	38.40	31.96
3. Percent hard seed	0.90	2.18
4. Hundred-seed weight (g)	17.69	16.83
5. Hundred-seed volume (cc)	14.66	14.02
6. Seed density (g/cc)	1.21	1.20
7. Seed specific gravity index	19.48	46.61
C. Structural components		
1. Plant height (cm)	52.31	48.68
2. Primary branches/plant	6.01	2.59
3. First internode length (cm)	4.46	3.74
4. Nodes/main stem	14.05	8.45
D. Phenological traits		
1. Days to maturity	119.46	103.44
E. Physiological traits		
1. Pod potential/node	1.87	2.08

Hence, for increasing the soybean productivity, micro-environment prevailing in the vicinity of individual plant, both below and above the soil, needs attention.

Ideal plant type for intercropping: In the light of the question raised, concerning the development of ideotype under monocropping and their suitability for intercropping (Okibago, 1975; Gupta et al., 1978), it would be desirable to consider the information obtained from monoculture and intercropping systems at Palampur. Results obtained by overall ranking the different genotypes in both the systems (Table 2) clearly confirm the earlier doubts raised about the researches conducted in monoculture and their suitability in intercropping. It is evident, from Table 2, that genotype 36 is the first ranking genotype in monoculture but it gets only 28th rank in intercropping. The highest yielding genotype 27 in intercropping gets the 2nd rank in monoculture.

The critical examination of differential behavior of these genotypes under different cropping system (Table 3) reveals that the superiority of genotype 27 has been maintained in both the cropping systems, mainly due to least influence of intercropping on its plant height, whereas genotype 36 could not maintain its superiority in intercropping due to appreciable reduction of its plant height.

High yield of genotype 27 in intercropping also appears to be due to its largest petiole length and high pod potential per node as well as per main stem. Although plant height for genotype 27 has remained constant in both the systems, number of nodes per main stem has been considerably reduced in intercropping system and the degree of reduction is more or less same as that of genotype 36, which has shown differential behavior with respect to yield under different cropping systems. This again confirms the importance of higher nodes for high yields as there was in general reduction of number of nodes per main stem and invariably, thus, leading to considerable reduction of yield under intercropping as compared to monoculture. More or less similar trend was evident for other genotypes having differential response. Hence, it appears that to have a suitable genotype of soybean for intercropping system, the soybean plant is to be tailored with higher number of pods per main stem. This can be achieved by having a plant ideotype with a tall monobranch; and tallness is to be obtained, not by increasing the internode length, but by increasing the number of nodes.

Table 2

Relative ranks of 40 genotypes in monoculture and intercropping at Palampur with respect to seed yield

Genotypes	Monoculture	Intercropping
1	10	14
2	27	12
3	25	25
4	34	7
5	13	27
6	24	36
7	35	20
8	22	38
9	29	34
10	37	37
11	39	33
12	5	35
13	38	17
14	8	39
15	4	2
16	6	23
17	30	18
18	23	30
19	11	19
20	3	29
21	33	3
22	31	15
23	26	24
24	7	8
25	14	4
26	15	22
27	2	1
28	16	16
29	17	26
30	12	31
31	36	40
32	19	32
33	21	9
34	20	5
35	28	6
36	1	28
37	18	10
38	32	11
39	40	21
40	9	13

Table 3

Differential response of the highest yielding genotypes in different cropping systems

Characters	Genotypes			
	36		27	
	Mono-culture	Inter-cropping	Mono-culture	Inter-cropping
1. Seed yield/plant (gm)	11.42	0.90	10.79	2.48
2. Pods/plant	36.60	9.50	32.60	10.30
3. Pods/main stem	5.40	5.90	5.40	6.20
4. Seeds/pod	2.40	1.60	2.70	1.70
5. Hundred-seed weight (gm)	16.49	16.69	18.44	17.25
6. Plant height (cm)	52.40	42.21	55.85	52.95
7. Primary branches/ plant	8.80	2.50	7.70	3.30
8. Nodes/main stem	16.60	8.90	16.80	9.40
9. Pod potential/node	2.30	1.70	1.50	2.50

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4) Variation for seed yield, its quality and nutritional traits in soybean.

To bring about genetic improvement for any economic trait in economic plants, the foremost prerequisite is the presence of sufficient amount of genetic variability for the trait under improvement in the organism to be improved. In the present investigation, an attempt has been made to get the information on nature and magnitude of variability for various seed quality traits along with seed yield traits in the soybean germplasm maintained at the Himachal Pradesh Agricultural University, Palampur.

Materials and methods: The material for the present study consisted of 250 diverse genotypes of soybeans of both indigenous and exotic origin, and 5 standard checks. The test cultures, along with checks, were grown in augmented design in 4 m rows, 50 cm apart. The plants were spaced at 10 cm. The checks were sown after every 10 test cultures in random manner. The crop was raised during summer, 1978, at departmental farm, Himachal Pradesh Agricultural University, Palampur. The seeds were harvested from random plants of each check and test culture, and were evaluated for characters namely: seed yield per plant, number of seeds per plant, seed weight, seed volume, water absorption capacity, percent germination, percent hard seeds, specific gravity index, boldness index, crushing hardness, percent moisture, percent protein, percent phosphorus and potassium percentage. Percent protein, phosphorus and potassium were estimated as per the procedure given by Li (1966), Jackson (1973) and A.O.A.C. (1976), respectively. The data were analyzed as per the model given by Federer (1955).

Table 1

Analysis of variance for augmented design for

14 characters studied in soybean germplasm

Source + Characters	Mean square due to				
	Blocks (ignoring entries)	Entries (eliminating blocks)	Varieties (checks)	Checks and test cultures vs. test vars.	Intra-block error
Seed per plant	5726.10*	960.46 *	308.26	970.89*	216.16
Yield per plant (g)	72.31	33.40	154.61	31.46	176.80
Seed weight (mg)	2249.92*	2199.96*	3786.64*	2174.57*	247.62
100 seed volume (cc)	17.15*	13.40*	17.96*	13.33*	1.03
Water absorption (cc)	151.66	102.94	1723.30	77.02	1507.02
Percent germination	2142.67*	234.75	345.96	232.97	147.77
Percent hard seeds	98.41*	51.56*	0.80	52.372*	0.27
Crushing hardness (kg)	278.99*	7.649	22.42	7.41	9.22
Percent protein	88.05*	31.03*	103.99*	29.86*	11.94
Percent potassium	0.145*	0.09*	0.07	0.09	0.04
Percent phosphorus	0.02*	0.01	0.00	0.01	0.006
Percent moisture	19.07*	6.00*	0.90	6.03*	3.00
Boldness index	0.64	0.62	0.45	0.62	0.32
Specific gravity	703.21	739.56*	674.24	740.61	323.54

+Degree of freedom for blocks ignoring entries, entries eliminating blocks, checks and test cultitures vs. test vars. Intrablock errors are 4, 254, 4, 250, 16, respectively.

*Significant at the 5% level.

Results and discussion: The analysis of variance (Table 1) indicates that, in the material under study, sufficiently large amount of genetic variability is present for seed weight, 100-seed volume, percent hard seeds, percent protein, percent seed potassium, percent seed moisture and specific gravity index, besides seeds per plant. Various earlier workers also have reported the presence of sufficient genetic variation for these traits in soybean (Weatherspoon and Wentz, 1934; Weber, 1950, Smith and Weber, 1968, Fehr and Weber, 1968; Arora et al., 1970; Gopani and Kabaria, 1970; Kaw and Menon, 1972; Gopani et al., 1972; Kwon, 1972; Shiv et al., 1972; Verma et al., 1972; Lee, 1977; Joshi and Smith, 1978; Shettar et al., 1978; Gupta and Garg, 1980; Gupta et al., 1980; Srinives and Hadley, 1980; and Jaranowski et al., 1980).

For percent potassium content, the information on genetic variation in literature is as good as nil. However, Beeson (1941) reported the variation present for this trait in the form of range without indicating the nature of variation, whether it was due to genetic or environmental causes. In the present material, the results clearly indicate that genotypic differences do exist for percent potassium content in soybean.

For percent germination score, which is a very important trait and needs immediate genetic manipulation for its improvement in order to provide better field stand for obtaining stable increased production in the country, sufficient genetic variability does not appear to exist in the material investigated in the present study. In the literature as well, the information on genetic variability for this trait is very limited. It is only recently that Tiwari et al. (1978) and Gupta and Garg (1980), have reported the presence of genetic variability for this trait in soybean. For boldness index, crushing hardness and water absorption, analysis of variance indicates absence of sufficient genetic variability in the present material. For these traits, the information available on genetic variability in literature is scant. However, for phosphorus content, some information in the form of range has been reported by earlier workers, namely, Dollier et al. (1940) and Beeson (1941), but none of them have tried to find out the nature of variability with respect to the causal factors - genetic vs. environmental. In the present material, a wide range of variability (0.19 to 0.74%) has been recorded, but the variation appears to be mostly environmental. For crushing hardness, Gupta et al. (1980) reported significant genetic differences in photoperiod-insensitive

Table 2

The mean, range and promising genotypes for 14 characters studied among 250 test cultures of soybean

Characters	Mean	Range	Genotypes exhibiting mean performance		
			Highest	Lowest	Other promising
Seeds per plant	73.17	30.20-196.50	Himso 76	Himso 16	Himso 302, Himso 29, Himso 409, Himso 772
Yield per plant (g)	10.88	2.45- 30.28	Himso 772	Himso 430	Himso 29, Himso 127, Himso 368, Himso 365
Seed weight (mg)	151.24	40.00-315.00	Himso 26	Himso 81	High seed wt.: Himso 16, Himso 308, Himso 304, Himso 440 Low seed wt.: Himso 76, Himso 78, Himso 427, Himso 84
100 seed volume (cc)	13.16	4.00- 22.00	Himso 308	Himso 81	Himso 304, Himso 442, Himso 440, Himso 365, Himso 375
Water absorption (cc)	18.58	4.00- 39.00	Himso 304	Himso 81	Himso 308, Himso 283, Himso 357, Himso 365
Percent germination	75.23	18.00- 99.00	Himso 458	Himso 273	Himso 123, Himso 302, Himso 65, Himso 409, Himso 427, Himso 78
Percent hardness	2.62	0.00- 55.00	Himso 384 Himso 389	145 Genotypes with no hard seeds	High hard seeds: Himso 443, Himso 37, Himso 38 Low hard seeds: 145 genotypes with no hard seed

Table 2 - *Continued*

Characters	Mean	Range	Genotypes exhibiting mean performance		
			Highest	Lowest	Other promising
Crushing hardness (kg)	16.85	9.60- 27.80	Himso 430	Himso 341	Himso 17, Himso 776, Himso 14, Himso 460
Percent protein	34.72	21.30- 48.50	Himso 778	Himso 395	Himso 389, Himso 331, Himso 463, Himso 494
Percent potassium	1.24	0.48- 2.92	Himso 278	Himso 375	Himso 328, Himso 119, Himso 16, Himso 366
Percent phosphorus	0.41	0.19- 0.74	Himso 400	Himso 43	Himso 63, Himso 53, Himso 16, Himso 388
Percent moisture	6.04	0.03- 18.69	Himso 452	Himso 44	High moisture: Himso 451, Himso 70, Himso 421, Himso 335 Low moisture: Himso 272, Himso 64, Himso 57, Himso 426
Boldness index	4.80	2.55- 6.51	Himso 316	Himso 78	Himso 283, Himso 347, Himso 771, Himso 102
Specific gravity	49.95	0.00- 98.00	Himso 333	Himso 368	Himso 67, Himso 109, Himso 352, Himso 366

group of soybean and not in photoperiod-sensitive group. Their results further indicate greater influence of environmental effects for crushing hardness as observed in the present material. For water absorption and boldness, there is hardly any report in the literature.

To exploit the observed wide range of variability for some of the economic traits, studied in the present material, it might be desirable to look at the individual genotypes from the point of view of their utility in the practical breeding program. The promising genotypes, which can be used in hybridization programs, have been summarized in Table 2. However, the detailed data with respect to 250 genotypes studied for each trait have been documented by Kalia (1980). In this table, mean and range for each character also have been given. This table reveals some interesting characteristics about the promising genotypes.

'Himso 76', the best genotype for seeds per plant, is only second best for low seed weight. Himso 302 and Himso 409, second and fourth for seeds per plant, respectively, are third and fifth, respectively, for germinability. Himso 29 and Himso 772, third and fifth for seed number, respectively, are second and first, respectively for yield per plant. Genotype Himso 365, fifth in yield per plant, also holds the same position for 100-seed volume and water absorption. Himso 308, third for high seed weight, is first in 100-seed volume and second in water absorption. Himso 304, fourth among high seed weight genotypes, holds second position for 100-seed volume and first for water absorption. Genotype Himso 440, fifth for high seed, and second best for high boldness index, is third best for water absorption. Another interesting genotype, Himso 389, with highest number of hard seeds, is only second best for protein content. Genotype Himso 16, second for high seed weight, is fourth for both potassium and phosphorus content. Himso 78, a small seeded genotype, is also among best five for germination. Himso 366, being fifth for high potassium content, is also fifth for specific gravity index. Genotype having desirable combinations of traits can be exploited through selection.

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1) Breeding soybean varieties for the northern India.

Soybean has been under cultivation in low hills of Kumaon and Garhwal regions of the Himalayas and the foot hills for ages. However, the old varieties were generally late, had viny growth habit, freely shattering pods and gave low yields. The crop got tremendous boost with the start of soybean breeding program in 1968 at this university. Taking the problems of this area into account, the breeding objectives have been sharply defined as given below:

1) High seed yield (30-40 q/ha).
2) Optimum maturity (90-105 days for the hilly areas and 110-120 days for the plains).

3) Disease resistance particularly to yellow mosaic virus, bacterial pustule, rhizoctonia aerial blight and rust.
4) Better seed quality (ability to germinate under adverse conditions and viability under normal storage).
5) Plant type (semi-dwarf, non-lodging, non-shattering type for pure stand and early, shade-tolerant, erect type for mixed cropping).

The following parental lines (Table 1) serve as a base material to generate variability for the above objectives, and the crossing nursery is being gradually supplemented by the new breeding lines.

Table 1

Crossing nursery

Parental line	Important character
UPSM-534	Immune to yellow mosaic
Glycine formosana	Immune to yellow mosaic
Bragg	Good plant type, high seed yield, resistant to bacterial pustule
Alankar	High seed yield, tolerant to yellow mosaic, better seed quality
Ankur	Tall, rapid initial growth, resistant to rust, better in germination, maintains seed viability even if stored at room temperature
Kalitur	Good germinability, high adaptability
UPRI-1	Heavy and broad foliage, profuse podding, resistant to caterpillar under natural conditions
PK-308	Narrow leaflet, high seed yield
Shilajeet	Dwarf, early, moderately resistant to yellow mosaic, bacterial pustule and rust
PK-262	Medium height, sturdy plant, more pods/plant, early maturity
T-49	Good germination, high adaptability

The segregating generations resulting from simple F_1's are handled by pedigree method. The F_1's, where *G. formosana* is one of the parents, are back-crossed with the agronomically superior parent and then the material is routed through pedigree method of breeding. This back-crossing helps in

Table 2

Handling of the segregating generations

Generation	No. of progeny rows grown (5 m long)	No. of progeny rows selected	No. of progeny rows bulked	No. of selected plants/ progeny row	Characters for which selection practiced
F_1	1				
F_2	400-800 plants	100 plants	--	--	Height, maturity, resistance to diseases, shattering
F_3	100	15	--	10	As above + lodging, pods/ plant
F_4	150	15	--	15	As above + seed size (medium seed size preferred)
F_5	225	15	5	20	As above + seed coat color (yellow desirable)
F_6	200	15	10	25	As above + yielding ability
F_7	125	15	15	--	As above

concentrating the desirable genes in the segregating populations (Singh, 1975). The current breeding program, geared to meet the objectives outlined here, has come to an operational stage, as detailed in Table 2.

The numbers given are the average numbers. Actual numbers of the progeny rows grown and selected may vary depending upon the nicking ability of the parental lines. A progeny is bulked and considered to be a pure breeding line as soon as all the plants appear to be uniform for easily observed morphological and seed characters. Any uniform progeny may be sometimes bulked as early as F_3 (Love, 1927). However, Hays and Garber (1927) do not consider bulking any progeny lines before F_5. We start bulking some of the progenies in F_5 and continue up to F_7 based on foliage, height, maturity and seed color uniformity.

This program throws out about 300 new breeding lines, which are evaluated in about 15 station trials each, in a randomized block design with two replications. Each trial consists of 18 new lines and two common checks, i.e., 'Bragg' and 'Alankar'. The lines outyielding the checks (about 80-90) are again evaluated in five separate trials each, in a randomized block design with four replications, having 18 new lines and two common checks, Bragg and Alankar. During evaluation, each plot consists of 5 rows, 5 m long, spaced 60 cm apart. Based on evaluation of germplasm lines and execution of the breeding program as described here, it has been possible to release four soybean varieties: Bragg (introduction from USA), 'Ankur', Alankar and 'Shilajeet' (all developed by B. B. Singh) for the northern hill and plain zones of this country. Many superior lines, producing about 30-35 q/ha (seeds) in 115-125 days, are in the advance stage of testing under coordinated soybean improvement project. These lines are PK-262, PK-271, PK-308, PK-327, and PK-330. The soybean breeding program is fully geared to meet the future challenges.

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2) Pod setting under standard crossing procedures in soybean.

The success in artificial crossing in soybean is generally poor. Each breeder uses his own imagination and refinements in the technique of crossing. The standard emasculation and pollination procedure as described by Johnson and Bernard (1963) and Paschal (1975) is being followed at this center. This appears to be quite convenient and fast and we are reporting the extent of crossed pod setting under our conditions, based on thousands of buds emasculated and pollinated during rainy season 1980-81. This may help other breeders in planning the number of crosses to be attempted for genetical and breeding programs.

Flower buds (color of petals had just started appearing) were selected for emasculation. Lobes of calyx were removed by pulling downward with forcep. Corolla was then grasped with the forcep at a right angle to the axis and all five petals were simultaneously removed by giving a gentle whirl movement upwards. During this process, sometimes anthers were also removed. If some of the anthers were left, they were removed in the subsequent pulls. The pollination was done immediately after emasculation both in forenoon and afternoon. The staminal column was removed from the freshly open flower and used as a brush to apply pollen to the stigma. Crossing was carried out from August to October by 6 persons. The results are given in Table 1.

The crossed pod setting ranged from 7.22 to 15.36%, with an overall average of 10.26%. The variation from person to person was naturally due to difference in skill. This setting compares closely with an earlier finding of Saha (1970) who got 12% success. The setting was highest when crosses were made in October (17.88%), lowest in August (6.48%), and close to overall average in September (12.38%). Higher pod setting in October was primarily due to less rain (7 mm) and more sunshine hours (9 h) in October, as compared to higher rains (64.55 mm) and less sunshine hours (6.8 h) in August and September. Maximum average daily temperature in August, September

Table 1

Crossed pod setting

Person	No. of buds crossed	No. of crossed pods set	Crossed pod setting (%)
1	2603	345	13.25
2	2866	207	7.22
3	2237	205	9.16
4	1940	298	15.36
5	1807	169	9.35
6	2880	247	8.58
Total	14333	1471	10.26

and October was 33, 32 and 31°C, respectively. Nights in October were cooler (minimum temperature in October was 18°C as compared to 25 and 22°C in August and September, respectively). This could have been an additional factor for higher seed setting in October.

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1) Alteration in seed oil combustibility by a soybean chlorophyll mutant.

Crop farmers are understandably interested in use of vegetable products as petroleum substitutes. Much of this interest now centers around fuels for internal combustion engines. Use of "raw" or slightly modified seed oils as diesel fuel is attractive for a number of reasons: 1) oil extraction is a rather simple, straight-forward process; 2) the high-protein by-products are already being used in commercial animal feed supplements; and 3) energy and dollar cost balances are easily calculated, and seem to favor on-farm processing. Short of "breakthrough" increases in yields, commercial development of seed oil fuels for non-farm use is probably unrealistic. This is not to say that all vegetable oils have no promise for commercial development.

Essential to achieving efficient adaptation of vegetable oils as fuels for internal combustion engines will be alteration of engine design and secondary modification of vegetable oils themselves. Genetic modification is an option which, at present, holds unknown promise. Accumulation of experience with vegetable oil fuels will undoubtedly add to the present body of knowledge about desirable chemical qualities for breeders to guide on.

During my high school days in the 1950s, I worked extensively with pulse-jet engine design and combustion. Last fall, with a long leftover engine and test stand, I undertook a brief study of pulse-jet combustion character of seed oils from several soybean varieties and mutants.

The pulse-jet engine is literally "a horn that blows itself." With some acoustical complications, it is simply a tube with reed- or leaf-type valves and a fuel injection system at one end. A spark plug, a compressed air source, and an explosive-at-ambient-pressure fuel-air mixture are required for starting. Once started, compression and combustion are self-sustaining, and fuels with low volatility and high flash point can be substituted for the gasoline or propane "starter."

The engine I used in my tests consumes 15-20 gm of fuel per minute and generates 150 to 200 gm of static thrust. The measure of "combustion efficiency" used for comparison of raw seed oils was gm of thrust/gm of fuel/sec. An "emissions trap" consisting of a 2 lb coffee can stuffed with glass wool was placed into the exhaust path 20 cm from the engine nozzle. This trap was

dried in a 200°C oven for 15 minutes, weighed, "run" for one minute, dried for another 15 minutes, and reweighed to get a measure of "non-volatile" emissions.

I detected essentially no varietal differences in "combustion efficiency" or "emissions." To my surprise, however, one chlorophyll mutant (phenotypically similar to y_9, though of untested allelism) gave consistently higher (ca. 10%) combustion efficiency values and lower (ca. 15%) emissions values than all others tested, including the "normals."

I have enlisted the help of local college chemistry departments in comparing oil from this mutant with its parent line ('Williams'). At this point, I can only say that the mutant seems to have slightly lower than normal viscosity. If my measurements can be taken seriously, they indicate that genetic modification of seed oil fuels may indeed have a future. I would be happy to correspond directly with anyone about details and future developments (and seeds) on this matter.

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1) Interactions of cultural practices with insect-induced stress on soybeans.

Numerous reports exist which characterize yield loss and defoliation relationships. Management guidelines and decisions regarding defoliating pests have been based largely upon findings from one or more of those studies. The use of such studies as decision-making criteria may be limited since most defoliation/yield-related research has been conducted in the Midwest with varieties, growth habits and environmental conditions widely divergent from those found in other areas of production. Secondly, the work reported thus far has been developed on wide rows. Recently, narrow row plantings of soybeans have shown favorable responses in yield optimization studies and growers are shifting to this new cultural practice. Furthermore, there are indications that compensation ability of soybeans to defoliation stress may vary with row spacing. Therefore, the study reported here was the first of a series of experiments designed to refine defoliation thresholds for decision-making purposes under narrow row conditions. Specifically, attempts were made to quantify the interaction of row spacing with the compensation ability of soybeans to defoliation stress.

In 1979 and 1980, two varieties, 'York' and 'Delmar', were planted at three row spacings, 100 cm (40 in.), 76 cm (30 in.), and 18 cm (7 in.), in a split-split plot design with four replications as randomized blocks. Defoliation was achieved by removing 50% of the leaf area by the hole punch method (Pedigo and Hammond, 1978) at the R4-R6 stage of development. Data on seven yield and growth components were collected at harvest from samples of 10 plants in each defoliation x row spacing combination.

Though the data for 1980 have not yet been completely analyzed, some notable trends were present in 1979. The magnitude and direction of responses changed with row spacing and this interaction was similar for both varieties. Reductions in yield and growth components as a result of defoliation were greatest in the 76 cm spacing, intermediate in the 18 cm spacing and lowest in the 100 cm spacing. Only significant reductions in seed weight and number of nodes resulted in the 100 cm spacing which was apparently able to compensate for defoliation more than the other spacings.

According to basic ecologic and agronomic principles, the 18 cm spacing would be expected to have the greatest compensation capacity since it approximates equidistant spacing which maximizes resource utilization with minimum interplant competition. This is further reinforced by the fact that narrow spacings produce higher yields and have a higher leaf area index. However, the 18 cm spacing did not compensate as well as 100 cm but did compensate better than 76 cm spacings.

Thus far, an explanation is available in terms of light interception. The short interplant distance of the 76 cm and 100 cm plantings lends to greater leaf overlap and higher levels of interplant competition for light interception than in the 18 cm plantings. Furthermore, the canopy does not close in the 100 cm plantings and light interception is optimal, from three sides. As a result, the lower canopy of the 100 cm plantings has a greater function in production of photosynthates than in the 18 and 76 cm plantings. This optimal interception scheme could account for the high compensation ability of 100 cm plantings. Due to the distance between plants in the 18 cm plantings, there is a lesser degree of leaf overlap between plants and thus correspondingly less interplant competition for light interception in the upper canopy. The intermediate compensation of 18 cm plantings may be related to minimized interplant competition for light interception since a substantial portion of its upper canopy is free from such competition with adjacent plants. Coupled with other advantages of minimal resource competition which follows from equidistant planting, this may enable 18 cm plantings to compensate for a greater percentage yield loss than 76 cm ones. The relatively poor compensation within the 76 cm spacings can be accounted for by the presence of a high degree of interplant competition as in 100 cm plantings in addition to a closed canopy and reduced light interception in lower leaves as in 18 cm plantings. Another factor, on which data was collected in 1980 and which may be involved, is the degree of branching exhibited by the two varieties.

With increased yields in 18 cm plantings, a smaller percentage of the yield can be lost before economic damage is realized. If these trends are upheld through the complete analysis of the 1979 and 1980 data, then a necessity may exist for the development of new thresholds applicable to both types of planting practices. Increased yields of narrow rows are available. However, in order to achieve the available maximum potential yields and in light of the apparent differential compensation with row spacing, thresholds may need to be refined.

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1) Development of cyst nematode on different soybean varieties.

Soybean cyst nematode (SCN) has emerged as one of the most serious pests of soybeans. Over 80% of the cultivable area in southeast Missouri is infested with this organism. Several varieties resistant to SCN race 3 have been developed and released. These included 'Custer', 'Dyer', 'Mack', 'Pickett', 'Forrest', 'Centennial', 'Franklin', and 'McNair 770'. These varieties carried resistance from 'Peking'. However, Peking is not resistant to race 4. PI 88,788, which carries high degree of resistance to race 4, was the donor parent in the development of 'Bedford', J74-51 and D75-10710. Of these, Bedford and J74-51 (now called 'Nathan') have been released. D72-8927 derived its resistance apparently from Peking and PI 90,763 and was selected primarily for resistance to race 2 (personal communication with Dr. E. E. Hartwig).

Under greenhouse conditions, while screening against a mixture of SCN races, all the lines mentioned above show reproduction of at least few white females. This experiment was undertaken to study the rate of SCN population growth in the soil under several of these genotypes. The test was laid out in a randomized block design with 4 replications. The soil samples were taken after planting and at one month intervals, about 5 cm away from the plants. One hundred grams of soil was washed with an elutriator and cysts counted with the help of a stereo-microscope. The data are presented in Table 1.

During the first 2 months, there was only a slight increase in SCN population. This was probably due to the severe hot and dry weather prevailing during 1980. The population increased tremendously between August 1 and

Table 1

Effects of different genotypes on SCN populations

Variety	Number of cysts/100 grams of soil — Date of sampling — 1 June	1 July	1 Aug.	1 Sept.	1 Oct.	Yield B/A[†]
Essex	9	12	40	232	175	26.2 ce
Forrest	6	6	11	40	88	34.8 a
Peking	10	6	9	45	34	31.2 ac
Bedford	5	6	7	18	30	29.1 be
J74-51	15	14	10	41	51	28.8 be
D75-10710	7	10	7	9	25	25.2 de
D72-8927	12	17	20	43	75	23.6 e
Bedford 70% Forrest 30%	10	10	18	58	54	30.6 ad
Mean	7	10	15	61	66	

[†] Values that are followed by the same letter are not significantly different at the 5% probability level according to Duncan's new multiple range test.

September 1. Maximum increase of SCN population was observed under 'Essex', which is a susceptible variety. Peking, Bedford and J74-51 gave almost similar response. The higher population under J74-51 may be due to the presence of more cyst in the soil to start with. D75-10710 showed fewer cysts whereas D72-8927 had more cysts compared with that of Bedford. A mixture of 70% Bedford and 30% Forrest gave intermediate response to the two varieties.

We plan to run this test in the same plots for several years without rotation, to study disease epidemiology and to see for how many years the same variety can be grown in a field without appreciable loss in yield.

S. C. Anand

2) Genotype response to soybean cyst nematodes in different soil sources.

Soybean cyst nematode was first observed in North Carolina as a pest on soybeans in 1954. Within a few years, it was reported from Virginia, Tennessee, Arkansas, Missouri and Illinois. This necessitated the screening of the soybean germplasm, which lead to the discovery of the following lines carrying resistance to SCN. These are, 'Peking', PI 88,788, PI 84,751, PI 89,772, PI 90,763, PI 87,631-1, PI 209,332 and 'Cloud'. Of these, Peking was used as donor parent for race 3 resistance and PI 88,788 as donor for race 4 resistance. Very little is known about other lines, whether they carry same or different factors for resistance. All these lines (except PI 84,751) along with 'Essex', 'Forrest' and 'Bedford' were tested in the greenhouse against 3 different sources of soil. In the Clarkton soil, Essex was grown for the last two years (1979 and 1980), Sikeston soil had Bedford in 1979 and Forrest in 1980, Kewanee soil had Bedford in 1979 and 1980. One plant was grown in a 7½ cm pot in each soil and the number of cysts (white females) were washed and separated from the roots 30 days after planting. The cysts were counted with the help of a stereo-microscope. There were 3-5 replications for each line. The data are presented in Table 1.

The number of cysts per plant on Essex (susceptible check) varied considerably. This was due to the presence of different number of cysts in each soil sample. Forrest, which carries genes for resistance from Peking, always had a higher count which indicated that Peking has some additional genes for resistance. Based on the cyst-count, Bedford has almost same degree of resistance to SCN as PI 88,788. The Clarkton data showed that PI 89,772 and PI 90,763 were less resistant, whereas Kewanee data indicated these two lines to be more resistant compared with PI 88,788. It is likely that planting of Bedford two years in a row increased the frequencies of pathotypes virulent on it. It seems that PI 89,772 and PI 90,763 carry greater degrees of resistance to those pathotypes which reproduce on Bedford or PI 88,788. PI 87,631-1 and PI 209,332 showed response similar to that of PI 88,788. Cloud was more susceptible than other lines.

More than 1500 new PI lines were screened against SCN using soil from Clarkton. PI 416,762 was the only one which was found to have high resistance to a mixture of races. This line is viney and has black seed coat.

Table 1

Number of cysts per plant

	Source of soil					
	— Clarkton —		— Sikeston —		— Kewanee —	
		% of Essex		% of Essex		% of Essex
Essex	114	100	283	100	27	100
Forrest	104	91	242	85	15	55
Peking	41	36	67	31	3	11
Bedford	12	10	53	19	12	44
PI 88,788	8	7	21	7	10	37
PI 89,772	35	31	31	11	5	2
PI 90,763	21	18	35	12	1	4
PI 87,631-1	10	9	32	11	12	44
PI 209,332	12	10	17	6	12	44
Cloud	82	72	94	33	20	74
PI 416,762	--	--	20	7	--	--

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3) New races of cyst nematodes

Physiological strains of soybean cyst nematode (SCN) were first reported by Ross (1962). Later a new biotype was observed in Arkansas (Riggs et al., 1968). The SCN pathotypes then known were classified into four races based on their ability to reproduce on a set of soybean differentials (Golden et al., 1970). Recently a soil sample was collected from the West Tennessee Agricultural Experiment Station, Jackson, TN from a field where 'Bedford' or other lines derived from the crosses involving PI 88,788 were grown for 5-6 years. This soil sample had 18 cysts/100 gms of soil. The three differentials, 'Peking', PI 88,788, PI 90,763 along with 'Essex' and PI 89,772 were screened against this soil sample in 3" pots. The number of cysts per plant root were observed 30 days after planting and index of parasitism was calculated using Essex as the susceptible host (instead of 'Lee') as described by Golden et al. (1970). The results are presented in Table 1.

Table 1

Reaction of various soybean differentials to races of cyst nematodes

Population	Differentials						Race
	Lee	Peking	Pickett	PI 88,788	PI 90,763	PI 89,772	
	+	-	-	+	-		1[a]
	+	+	+	+	-		2[a]
	+	-	-	-	-		3[a]
	+	+	+	+	+		4[a]
TN-79	+[b] (100%)	- (4%)	+ (27%)	+ (38%)	- (4%)	- (2%)	5
P4	+ (100%)		+ (66%)	- (3%)	+ (23%)	+ (16%)	6

[a]As described by Golden et al., 1970.

[b]Used Essex instead of Lee.

+Number of white females 10% or more of the number on Lee or Essex.

-Number of white females less than 10% of the number on Lee or Essex.

The new isolate designated TN-79 did not match any one of the 4 races described earlier (Golden et al., 1970). It is different from race 1, as it reproduces on 'Peking'. A similar isolate was reported from Japan by Inagaki (1978) and classified as race 5. The SCN collected in Minnesota produced similar response on the four differentials (MacDonald, 1980). Another isolate of SCN (P4) was developed by repeated reproduction and selection of nematode on PI 89,772. This isolate produced a + reaction on PI 90,763 and a - reaction on PI 88,788. Such reactions have not been reported so far and this isolate could be classified as race 6.

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1) Soybean linkage tests with ms_2

In the last decade, at least four independently inherited, nuclear recessive genes for male sterility (ms_1, ms_2, ms_3, ms_4) in soybeans have been discovered (Brim and Young, 1971; Bernard and Cremeens, 1974; Palmer, 1979; Palmer et al., 1980). The successful exploitation of genetic male sterility in soybean breeding programs requires that male-sterile plants be readily distinguishable from male-fertile sibs. At present, soybean male steriles are conveniently distinguishable from male-fertile sibs only after pod development, when the reduced pod set and delayed physiologic maturity of male-sterile plants become evident. Even then, misclassification is possible when disease reduces pod set on male-fertile plants, or when conditions favor pollen transfer to enhance pod set on male-sterile plants.

Classification of male-sterile and male-fertile plants could be facilitated more conveniently with the use of a genetic marker that was tightly linked with a male-sterile gene, provided that the marker gene conditioned easily recognizable phenotypes, preferably expressed prior to flowering to permit rogueing prior to pollination. At present, the only known linkage with a genetic male sterile is ms_1 with w_1 (flower color) with a recombination value of $29.7 \pm 1.6\%$ (Palmer, 1977). The objective of this investigation was to search for a genetic marker tightly linked with the ms_2 gene in soybeans.

For all linkage crosses in this study, a backcross-derived near-isogenic line of the cultivar 'Williams', possessing the *ms*$_2$ gene, was used as the female parent, while several backcross-derived near-isogenic lines of the cultivar 'Clark', possessing the various selected marker genes, were used as the male parents. F_2-linkage results are presented in Table 1 for crosses involving various marker genes with *ms*$_2$. Linkage intensities were derived from the F_2-segregation data using the method of maximum likelihood to obtain recombination values and standard errors (Mather, 1951).

Of the 27 markers tested for linkage with *ms*$_2$ (Table 1), only four (*e*$_2$, *Lf*$_1$, *Pd*$_1$, and *y*$_9$) had calculated recombination values that were judged to be significantly less than 50%. Further examination of these four putative linkages by means of chi-square tests for goodness of fit between the *observed* F_2-class frequencies and the *theoretical* frequencies (expected on the basis of the calculated recombination values), indicated poor fits for the supposed linkages of *e*$_2$-*ms*$_2$ (χ^2 = 9.95, P < 0.01) and *y*$_9$-*ms*$_2$ (χ^2 = 1.50, P = 0.04). This suggested that the disturbance in the F_2-segregation ratios was due to factors other than linkage. Indeed, monogenic segregation ratios for *E*$_2$:*e*$_2$ phenotypes and *Y*$_9$:*y*$_9$ phenotypes were significantly different from an expected 3:1 segregation, indicating probable classification errors. Good fits were, however, obtained for the putative linkages of *Lf*$_1$-*ms*$_2$ (x^2 = 1.44, P = 0.49) and *Pd*$_1$-*ms*$_2$ (χ^2 = 1.50, P = 0.47). No reports of linkage of *Lf*$_1$ with *Pd*$_1$ were found in the literature. The presumed linkages of *Lf*$_1$-*ms*$_2$ and *Pd*$_1$-*ms*$_2$, if confirmed, are not tight enough, however, to be employed as a mechanism of distinguishing male-sterile and male-fertile plants.

Since Clark and Williams differed in flower color, F_2-linkage results for crosses involving the various marker genes with *w*$_1$ are presented in Table 2. Of the 25 markers, only *Ps* had a recombination value with *w*$_1$ that was judged to be significantly less than 50%. A chi-square goodness of fit test indicated a good fit of observed with theoretical frequencies expected, based on the calculated recombination value. Further linkage tests will be required to confirm this putative linkage of *Ps* and *w*$_1$.

Table 1

F_2 linkage test data for crosses involving 27 marker genes with the ms_2 gene for genetic male sterility

Genes	Phenotypic classes†					% Recombination	Linkage
Aa Bb	*AB*	*Ab*	*aB*	*ab*	Sum	± S.E.	phase *
Dt_1dt_1 Ms_2ms_2	175	53	39	21	288	57.4 ± 4.0	R
Dt_2dt_2 Ms_2ms_2	118	56	70	4	248	77.0 ± 6.0	C
Ff Ms_2ms_2	101	36	38	12	187	48.3 ± 5.6	R
Ss Ms_2ms_2	147	49	48	10	254	56.4 ± 5.0	C
E_1e_1 Ms_2ms_2	50	16	25	8	99	50.2 ± 7.6	C
E_2e_2 Ms_2ms_2	58	32	44	6	140	32.4 ± 7.5	R
E_3e_3 Ms_2ms_2	54	21	45	11	131	43.9 ± 7.0	R
Lf_1lf_1 Ms_2ms_2	124	40	32	22	218	39.7 ± 4.5	C
Lf_2lf_2 Ms_2ms_2	121	39	37	14	211	52.2 ± 5.0	R
Lolo Ms_2ms_2	70	16	32	9	127	51.3 ± 6.6	R
Lw_1lw_1 Ms_2ms_2	31	16	20	9	76	50.8 ± 8.5	R
P_1p_1 Ms_2ms_2	231	66	96	27	240	50.7 ± 3.7	C
$P_2p_2Ms_2ms_2$	40	17	14	6	77	50.3 ± 8.5	R
Pcpc Ms_2ms_2	160	56	37	16	269	52.5 ± 4.4	R
Pd_1pd_1 Ms_2ms_2	215	69	56	33	373	14.8 ± 3.5	C
Pd_2pd_2 Ms_2ms_2	46	13	10	4	73	44.8 ± 8.3	C
Psps Ms_2ms_2	91	27	30	8	156	51.4 ± 6.1	C
Y_3y_3 Ms_2ms_2	132	47	46	8	233	40.1 ± 5.4	R
Y_9y_9 Ms_2ms_2	173	53	83	12	321	38.8 ± 4.7	R
Ii Ms_2ms_2	67	43	29	19	158	52.3 ± 5.8	R
L_1l_1 Ms_2ms_2	207	71	80	28	386	49.7 ± 3.8	C
Rr Ms_2ms_2	80	35	36	9	160	42.5 ± 6.4	R
Tt Ms_2ms_2	246	92	68	34	440	46.2 ± 3.4	C
Tdtd Ms_2ms_2	249	65	65	18	397	51.7 ± 3.7	R
W_1w_1 Ms_2ms_2	3574	1163	1034	372	6143	48.6 ± 0.9	C
Wmwm Ms_2ms_2	50	16	14	5	85	51.6 ± 8.0	R
Nn Ms_2ms_2	164	66	47	16	303	44.9 ± 4.6	R

†*A* and *a* represent the appropriate dominant and recessive marker alleles, respectively; *B* and *b* represent Ms_2 and ms_2, respectively. *R represents a repulsion phase cross (*AAbb* x *aaBB*); C represents a coupling phase cross (*AABB* x *aabb*).

Table 2

F_2-linkage test data for crosses involving 25 marker genes with the w_1 for flower color

Genes	Phenotypic classes†					% Recombination	Linkage
Aa Bb	*AB*	*Ab*	*aB*	*ab*	Sum	± S.E.	phase*
Dt_1dt_1 W_1w_1	179	49	50	10	288	46.7 ± 4.6	R
Dt_2dt_2 W_1w_1	120	54	54	20	248	52.0 ± 4.9	C
Ff W_1w_1	117	20	35	15	187	61.6 ± 4.7	R
Ss W_1w_1	152	44	50	8	254	57.7 ± 5.1	C
E_1e_1 W_1w_1	49	17	27	6	99	56.6 ± 8.1	C
E_2e_2 W_1w_1	66	24	42	8	140	40.6 ± 7.0	R
E_3e_3 W_1w_1	60	15	44	12	131	48.7 ± 6.7	R
Lf_1lf_1 W_1w_1	116	48	40	14	218	52.4 ± 5.2	C
Lf_2lf_2 W_1w_1	120	40	40	11	211	47.3 ± 5.3	R
Lolo W_1w_1	74	12	34	7	127	49.8 ± 6.7	R
Lw_1lw_1 W_1w_1	36	11	23	6	76	45.0 ± 9.1	R
P_1p_1 W_1w_1	223	74	100	23	420	55.4 ± 3.9	C
P_2p_2 W_1w_1	40	17	17	3	77	37.8 ± 9.6	R
Pcpc W_1w_1	160	56	43	10	269	44.5 ± 4.9	R
Pd_1pd_1 W_1w_1	227	57	69	20	373	47.8 ± 3.8	C
Pd_2pd_2 W_1w_1	43	16	11	3	73	54.6 ± 9.2	C
Psps W_1w_1	99	19	25	13	156	36.6 ± 5.1	C
Y_3y_3 W_1w_1	139	40	46	8	233	43.4 ± 5.3	R
Y_9y_9 W_1w_1	187	39	66	29	321	59.3 ± 3.7	R
Ii W_1w_1	79	31	38	10	158	44.4 ± 6.3	R
L_1l_1 W_1w_1	208	70	84	24	386	52.4 ± 3.9	C
Rr W_1w_1	98	17	36	9	160	53.5 ± 5.7	R
Tdtd W_1w_1	226	88	62	21	397	47.6 ± 3.9	R
Nn W_1w_1	175	55	52	21	303	53.5 ± 4.1	R
Tt W_1w_1	252	86	82	20	440	54.7 ± 3.8	C

†*A* and *a* represent the appropriate dominant and recessive marker alleles, respectively; *B* and *b* represent W_1 and w_1, respectively. * R represents a repulsion phase cross (*AAbb* x *aaBB*); C represents a coupling phase cross (*AABB* x *aabb*).

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1) Amylase and acid phosphatase genotypes of *Glycine max, Glycine soja* and *Neonotonia wightii*.

Three amylase loci, Am-1, Am-2, and Am-3, have been identified by electrophoresis (Gorman and Kiang, 1978). The activity of amylase at Am-1 and Am-2 is very weak, and that at Am-3 is much stronger. Based on heat lability and chemical reaction, Reiss (1978) concluded Am-1 and Am-2 represent α-amylase and Am-3 β-amylase. The Am-3 locus has four electrophoretic variants, namely, fast (F, rf = .51), slow (S, rf = .41), null 2 (S^2 slow with weak activity), and null 1 (n_1) (Gorman and Kiang, 1977, 1978; Kiang, 1980, and unpublished data). These four variants appear allelic only with regard to Am-3 with F and S codominant, S^2 recessive to F and S, but dominant over n_1 (Kiang, 1980, 1981; Hildebrand and Hymowitz, 1980b).

Soybean-variety-specific acid phosphatase electrophoretic zymograms were reported (Gorman, 1976). No variation was observed for the first and second zymogram bands. The third band (AP-3) displayed three mobility variants, fast (F, rf = .53), intermediate (M, rf = .48), and slow (S, rf = .45) (Gorman and Kiang, 1977). The three variants were found to be controlled by three codominant alleles at a single locus (Gorman, 1976; Hildebrand et al., 1980).

Seeds used in this project were obtained from three sources: 1) R. L. Bernard, USDA, Urbana, IL provided all U.S. named cultivars [*Glycine max* (L.) Merr.], 20 *G. max* introductions each from China, Japan and Korea, 20 accessions each of *G. soja* Sieb. & Zucc. from China, Japan and Korea, and 20 accessions of *Neonotonia wightii* (Arnott) Lackey from Africa; 2) R. G. Palmer, USDA, Ames, IA provided 14 introductions of *G. max* from Belgium, one from Netherlands, and four accessions from Yugoslavia, 15 accessions of *G. soja* from Japan, 18 from USSR and four from Korea; 3) S. Shanmugasundaram, Asian Vegetable Research and Development Center, Taiwan, provided 12 cultivars of *G. max*, 42 accessions of *G. soja* from Korea, and five accessions of *Neonotonia wightii* from Taiwan.

Seeds from each cultivar or accession were examined for amylase and acid phosphatase activity by a polyacrylamide horizontal gel electrophoretic procedure described by Gorman and Kiang (1977). This report does not include acid phosphatase genotypes of named U.S. soybean cultivars since acid phosphatase genotypes of cultivars in the USDA soybean collection have been reported (Hildebrand and Hymowitz, 1980a). For amylase we only report Am-3 genotypes since little variation in Am-1 and Am-2 has been found.

Amylase genotypes of *G. max* named cultivars are presented in Table 1. For acid phosphatase we only report on band 3 (AP-3). Amylase and acid phosphatase genotypes for *G. max* introductions from China, Japan, Korea, and Taiwan are presented in Table 2, those of *G. soja* in Table 3, and those of *N. wightii* in Table 4.

The results clearly indicate the high cultivar purity of soybean seeds. About 0.42% of heterozygous seeds for Am-3 locus, and 0.39% of heterozygous seeds for AP-3 locus were observed in the cultivated soybeans. Gorman (1976) observed 0.37% heterozygous seeds for Am-3 locus among 1361 cultivated soybean seeds. These heterozygous seeds are the products of natural outcrossing.

More heterozygous seeds were observed in *G. soja* seeds, particularly seeds from Japan and Korea. We detected 4.3% of heterozygous seeds for Am-3, and 0.84% for AP-3 from Japanese accessions; 2.5% and 1.85% of heterozygous seeds for Am-3 and AP-3 respectively from Korean accessions. Except for USSR introductions, *G. soja* also showed a higher degree of average polymorphism for Am-3 (13%) and AP-3 (7.1%) compared with *G. max* (Am-3, 1.1%).

We observed a fourth variant at the AP-3 locus in *G. soja* whose mobility is faster than the *F* variant previously reported. We used *VF* to represent

this variant (very fast), and its rf with respect to methyl blue was .57. This fourth variant is probably a codominant allele with the other three codominant alleles since one seed showed a 2-band pattern representing a heterozygote for the *F* and *VF* alleles.

More cultivars in *G. max* are fixed for the *F* allele at the Am-3 locus (86.6%) and for the *M* allele at the AP-3 locus (89.8%). However, in *G. soja* the genotypes are more evenly distributed for *F* and *S* alleles at Am-3 and for *F*, *M*, and *S* alleles at AP-3 locus except for 18 USSR collections, all of which were fixed for the *F* alleles at both the Am-3 and AP-3 loci.

Seeds of *Neonotonia wightii* did not show any amylase activity, except for 2 accessions from South Africa, which showed weak activity with *F* mobility (F^W). The zymograms of acid phosphatase in *N. wightii* are very different from *Glycine max* and *G. soja*. At least two different acid phosphatase zymograms have been observed in *N. wightii* accessions. These have simply been reported as type 1 or type 2. We are currently researching acid phosphatase in other glycine species as well as *N. wightii* and will be reporting the results separately.

Table 1

Amylase genotypes Am-3 of named U.S. soybean cultivars

Cultivar	Maturity group	Am-3	Cultivar	Maturity group	Am-3
A-100	I	*F*	Evans	0	*S*
Acme	00	*S*	Fabulin	IV	*F*
Adams	III	*F*	Fiskeby	00	*F*
Adelphia	III	*F*	Flambeau	00	*F*
Agate	00	*F*	Ford	III	*F*
AK	IV	*F*	Fuji	III	*F*
Aksarben	II	*F*	Funk Delicious	IV	*F*
Altona	00	*F, N*	Funman	II	*F*
Amsoy	II	*S*	Giant Green	I	*F*
Anoka	I	*F*	Gibson	IV	*F*
Aoda	IV	*F*	Goku	II	*F*
Bansei	II	*F*	Goldsoy	0	*F*
Bavender A	III	*F*	Granger	III	*F*
Bavender B	III	*F*	Grant	0	*F*
Bavender C	III	*F*	Green and Black	IV	*F*
Beeson	II	*S*	Guelph	III	*F*
Bethel	IV	*S*	Habaro	I	*F*
Black Eyebrow	II	*F*	Hahto Michigan	IV	*F*
Blackhawk	I	*F*	Hakote	II	*F*

Table 1 - *continued*

Cultivar	Maturity group	Am-3	Cultivar	Maturity group	Am-3
Bombay	I	*F*	Harbinsoy	IV	*F*
Bonus	IV	*S*	Hardome	0	*S*
Boone	IV	*F*	Hark	I	*F*
Burwell	I	*F*	Harly	I	*F*
Calland	III	*F*	Harman	III	*F, S*
Capital	0	*F*	Harosoy	II	*S*
Carlin	IV	*F*	Harosoy 63	II	*S*
Cayuga	I	F^{W}	Hawkeye	II	*F*
Chestnut	III	S^{W}	Henry	II	*F*
Chief	IV	*F*	Hidatsa	00	*F*
Chippewa	I	*F*	Higan	IV	*F*
Chusei	III	*F*	Hodgson	I	*F*
Clark	IV	*F*	Hokkaido	IV	*F*
Clay	0	*F*	Hongkong	IV	*F*
Cloud	III	*F*	Hoosier	I	*F*
Columbia	III	*F*	Illington	IV	*F*
Comet	0	*S*	Illini	III	*F*
Corsoy	II	*F*	Imperial	IV	*F*
Crest	00	*S*	Jefferson	IV	*S*
Custer	IV	*F*	Jogun	III	*F*
Cutler	IV	*F*	Kabott	0	*F*
Delmar	IV	*F*	Kagon	I	*F*
Disoy	I	*F*	Kanrich	III	*F*
Dunfield	III	*F*	Kanro	II	*F*
Earlyana	I	*F*	Kanum	II	*F*
Ebony	IV	*S*	Kent	IV	*F*
Elton	I	*F*	Kingston	IV	*F*
Emperor	IV	*F*	Kingway	IV	*F*
Etum	II	*F*	Korean	II	*F*
Kura	III	*F*	Peking	IV	*F*
Lee	VI	*F*	Perry	IV	*F*
Lincoln	III	*F*	Poland Yellow	0	*F*
Lindarin	III	*S*	Pollysoy	IV	*F*
Little Wonder	III	*F*	Portage	00	*S*
Macoupin	IV	*S*	Portugal	I	*F*
Madison	II	*F*	Pridesoy 57	I	*F*
Magna	II	*F*	Prize	II	*F*
Manchu	III	*F*	Protana	II	*F*
Manchu Hudson	II	*F*	Provar	II	*F*
Manchuria	I	*F*	Rampage	I	*F*
Mandarin	I	*S*	Renville	I	*F*
Mandell	III	*F*	Richland	II	*F*
Manitoba Brown	00	*F*	Roe	IV	*F*
Mansoy	III	*F*	Ross	III	*F*
Medium Green	I	*F*	Sac	I	*F*
Mendota	I	*F*	Sangor	IV	*F*
Merit	0	*F, S*	Sato-3	IV	*F*

Table 1 - *Continued*

Cultivar	Maturity group	Am-3	Cultivar	Maturity group	Am-3
Midwest	IV	*F*	Scott	IV	*F*
Miller 67	III	*F*	Seneca	II	*F*
Mingo	III	*F*	Shelby	III	*F*
Minsoy	00	*F*	Shiro	IV	*F*
Monroe	I	*S*	Sioux	00	*F*
Morse	IV	*F*	Sousei	II	*F, S*
Morsoy	00	*F*	Soysota	I	*F*
Mukden	II	*F*	Steele	I	*S*
Norchief	0	*F*	Tastee	II	*F*
Norman	00	*F*	Toku	II	*F*
Norredo	IV	*F*	Tortoise Egg	I	*F*
Norsoy	I	*F*	Traverse	0	*F*
Ogden	IV	*F*	Verde	III	*F*
Ogemaw	00	*F*	Viking	III	*F*
Ontario	I	*F*	Virginia	IV	*F*
Osaya	III	*F*	Waseda	II	*F*
Ottawa	I	*S*	Wayne	III	*F*
Pagoda	00	*S*	Wea	II	*F*
Pando	00	*F*	Willomi	III	*F*
Patoka	IV	*F*	Wilson	IV	*F*
Patterson	IV	*F*	Wolverine	III	*F*
			Yellow Marvel	II	*F*

Table 2

Seed amylase Am-3 and acid phosphatase AP-3 genotypes of soybean (*G. max*) introductions from China, Japan, Korea, Taiwan and Europe

Source		Maturity group	Am-3	AP-3
China	PI 103,080	IV	*S*	*S*
	103,088	III	*F*	*S*
	103,091	IV	*S*	*M*
	103,414	II	*F*	*M*
	103,415	IV	*S*	*S*
	103,419-1	IV	*F*	*F*
	123,577-2	IV	*F*	*M*
	135,589	II	*F*	*S*
	135,590	II	*F*	*M*
	158,765	IV	*F*	*M*
	232,987	II	*F*	*F*
	232,988	II	*F*	*S*
	232,989	II	*F*	*S*

Table 2 - *Continued*

Source		Maturity group	Am-3	AP-3
	232,990	II	*F*	*S*
	232,991	II	*F*	*S*
	253,650A	II	*F*	*M*
	253,650B	II	*F*	*F*
	253,651A	IV	*F*	*M*
	253,651B	IV	*S*	*F*
	253,652A	IV	*F*	*M*
Japan	124,871	IV	*S*	*S*
	181,531	0	*F*	*M*
	181,532	I	*F*	*M*
	181,533	II	*F*	*M*
	181,534	II	*F*	*M*
	181,535	III	*F*	*M*
	181,536	I	*F*	*S*
	181,537	II	*F*	*M*
	181,538	I	*F*	*M*
	181,539	IV	*F*	*M*
	181,540	III	*F*	*M*
	181,541	II	*F*	*M*
	181,542	III	*F*	*M*
	181,548	II	*F*	*M*
	181,549	III	*F*	*M*
	181,550	IV	*F*	*M*
	181,551	IV	*F*	*M*
	181,552	III	*F*	*M*
	181,553	III	*F*	*M*
	181,554	III	*F*	*M*
Korea	157,395	IV	*F*	*M*
	157,396	IV	*F*	*M*
	157,397	III	*F*	*M*
	157,398	IV	*F*	*S*
	157,401	IV	*F*	*F*
	157,402	IV	*F*	*M*
	157,404	IV	*F*	*M*
	157,405	IV	*S*	*M*
	157,408	IV	*F*	*M*
	157,409	IV	*F*	*M*
	157,410	IV	*S*	*F*
	157,414	IV	*F*	*M*
	157,416	III	*F*	*M*
	157,417	IV	*F*	*M*
	157,419	IV	*F*	*M*
	157,421	III	*S*	*S*
	157,424	IV	*S*	*M*
	157,428	IV	*S*	*M*
	157,429	III	*S*	*F*
	157,431	IV	*F*	*M*

Table 2 - *Continued*

Source		Maturity group	Am-3	AP-3
Taiwan	AV* 38		*F*	*M*
	57		*F*	*M*
	62		*F*	*M*
	66		*F*	*M*
	68		*F*	*M*
	69		*F*	*S*
	70		*F*	*M*
	73		*F*	*M*
	215		*F*	*M, S*
	5161		*F*	*S*
	2043		*F*	*M*
	2120		*F*	*S*
Netherlands	PI 132,201	I	N_1	*F*
Belgium	153,274	I	*F*	*M*
	153,275	O	*F*	*M*
	153,277	O	*F*	*M*
	153,278	O	*F*	*M*
	153,279	I	*F*	*M*
	153,282	I	*F*	*M*
	153,283	I	*F*	*M*
	153,284	O	*F*	*M*
	153,289	II	*F*	*S*
	153,292	III	*F*	*S*
	153,300	O	*F*	*M*
	153,304	O	*F*	*M*
	153,305	O	*F*	*M*
	153,306	O	*F*	*F*
Yugoslavia	248,395	O	*F*	*M*
	248,399	O	*F*	*M*
	248,407	I	*F*	*M*
	248,408	O	*F*	*M*

*AV represents Asian Vegetable Research and Development Center Collections.

Table 3

Seed amylase Am-3 and acid phosphatase AP-3 genotypes of *Glycine soja* from China, Japan, Korea and Russia

Source - Area		Maturity	Am-3	AP-3
China - 3	PI 65,549	II	*F*	*F*
- 3	135,624	II	*F*	*F*
- 4	163,453	VII	*F*	-*
- 3	391,587	II	*F*	*F*
- 3	407,288	II	*S*	*F*
- 3	407,289	II	*F*	*F*
- 3	407,290	II	*F*	*S*
- 3	407,291	II	*F*	*S*
- 3	407,292	II	*F*	*S*
- 3	407,293	II	*F*	*S*
- 3	407,294	II	*F*	*F*
- 3	407,295	II	*F*	*F, S*
- 3	407,296	II	*F*	*F*
- 3	407,297	II	*F*	*M*
- 3	407,298	II	*F*	*M*
- 3	407,299	II	*F*	*M*
- 4	407,300	V	*F*	*S*
- 4	407,301	V	*F*	*S*
- 4	407,302	V	*F*	*S*
- 4	407,303	V	*F*	*S*
Japan - 13	203,246	VII	*S*	*M*
- 17	342,434	V	*F*	*M*
- 17	366,122	IV	*S*	*M*
- 15	378,683	VI	*S*	*S*
- 15	387,684A	VI	*F*	*F*
- 15	387,684B	VI	*F*	*M*
- 14	378,685	VI	*S*	*M*
- 14	378,686A	VII	*S*	*F*
- 14	378,686B	VI	*F*	*F*
- 13	378,687A	VI	*F*	-
- 13	378,687B	VII	*S*	-
- 14	378,688	VII	*F*	*M*
- 15	378,689	VI	*S*	-
- 13	378,690	VII	*F*	-
- 13	378,691	VII	*S*	*F*
- 17	378,692	IV	*F*	*F*
- 17	378,693A	VII	*F*	*S*
- 17	378,693B	VII	*F, S*	*M*
- 15	378,694	VI	*S, F*	*M, F*
- 17	378,702	IV	*S*	*F*
-	406,684	?	*S*	*S*
- 16	407,019	V	*F*	*F*

*Dash represents unstudied seeds.

Table 3 - *Continued*

Source - Area			Maturity	Am-3	AP-3
Japan - 16	PI	407,020	V	*F*	*M*
- 16		407,025	V	*S*	*M*
- 16		407,037	V	*F*	*S*
- 16		407,042	V	*F, S*	*F*
- 17		407,048	V	*S*	*F*
- 15		407,054	VI	*F*	*S*
- 15		407,055	VI	*S*	*M*
- 15		407,062	VI	*F*	*F*
- 15		407,080	VI	*S*	*S*
- 15		407,083	VI	*F*	*F*
- 14		407,087	VI	*F*	*F*
- 14		407,107	VI	*F*	*VF*
- 15		407,286	VI	*F*	*M*
	AV*	5005		*F*	*M*
USSR - 1	PI	423,998	00	*F*	*F*
- 1		423,989A	0-00	*F*	*F*
- 1		423,989B	0-00	*F*	*F*
- 1		423,990	0-00	*F*	*F*
- 1		423,991	0-00	*F*	*F*
- 1		423,992	0	*F*	*F*
- 1		423,993	00	*F*	*F*
- 1		423,994	00	*F*	*F*
- 1		423,995	0-00	*F*	*F*
- 1		423,996	00	*F*	*F*
- 1		423,997	00	*F*	*F*
- 1		423,998	00	*F*	*F*
- 1		423,999A	0-00	*F*	*F*
- 1		423,999B	0-00	*F*	*F*
- 1		424,000	00	*F*	*F*
- 1		424,001	00	*F*	*F*
- 1		424,002	00	*F*	*F*
- 1		424,003	00	*F*	*F*
Korea	AV*	3080		*F*	*M*
		3081		*F, S*	*S*
		3083		*F*	-
		3084		*F*	*S*
		3085		*S*	*M*
		3086		*S*	*M*
		3087		*F, S*	*S, VF*
		3089		*F*	-
		3090		*F*	*F*
		3091		*F*	*S*
		3092		*S*	*M*
		3094		*F*	*F*
		3097		*F*	*M*
		3099		*F*	*S*

*AV represents Asian Vegetable Research & Development Center Collections

Table 3 - *Continued*

Source - Area			Maturity	Am-3	AP-3
Korea	AV*	3101		*F*	*S*
		3102		*F*	*M*
		3103		*F*	*F, M, S*
		3104		*F, S*	*S*
		3105		*F, S*	*F, S*
		3106		*F*	*F*
		3107		*F, S*	*F*
		3108		*S*	*VF*
		3109		*F, S*	*S*
		3110		*F*	*S*
		3111		*F*	*M*
		3112		*F*	*F, S*
		3113		*F, S*	*M*
		3114		*F*	*M*
		3120		*F, S*	*F*
		3122		*F*	*S*
		3123		*F, S*	*M*
		3124		*F, S*	*M*
		3125		*F, S*	*M*
		3126		*F, S*	*M*
		3128		*F*	*M*
		3130		*S*	*F*
		3132		*F*	*S*
		3133		*F, S*	*S*
		3136		*F*	*S*
		9055		*F*	-
		9056		*F*	*S*
		9057		*F*	*S*
		9058		*F*	*S*
Korea - 5	PI	339,731	V	*F*	*S*
- 5		339,732	IV	*S*	*S*
- 5		339,733	V	*F*	*M*
- 5		339,735A	IV	*F, S*	*F, S*
- 5		339,735B	IV	*S*	*S*
- 12		339,871A	V	*S*	*F*
- 12		339,871B	V	*F*	*F*
- 11		349,647	V	*S*	*S*
- 11		407,159	V	*F*	*M*
- 11		407,160	V	*S*	*M*
- 11		407,161	V	*F*	*M*
- 11		407,162	IV	*F*	*F*
- 11		407,163	V	*F*	*M*
- 11		407,164	V	*F*	*S*
- 11		407,165	V	*F*	*S*
- 11		407,166	IV	*F*	*M*
- 11		407,167	V	*F*	*M*
- 11		407,168	V	*F*	*M, S*
- 11		407,169	V	*F*	*S*

*AV represents the Asian Vegetable Research & Development Center Collections.

Table 3 - *Continued*

Source - Area		Maturity	Am-3	AP-3
Korea - 11	407,170	V	*F*	*F*
- 5	407,180	V	*S*	*F*
- 5	407,182	IV	*F*	*F*
- 11	407,185	V	*F*	*F*
- 11	407,188	V	*F*	*F*

*AV represents the Asian Vegetable Research & Development Center Collections.

Table 4

Seed amylase Am-3 genotypes of

Neonotonia wightii from Africa and Taiwan

Source		Am-3	A.P.*
Africa	PI 189,613	*N*	-
	224,976	*N*	2
	224,977	F^W	2
	224,978	F^W	2
	224,979	*N*	1
	224,980	*N*	1
	224,981	*N*	1
	230,322	*N*	2
	230,323	*N*	1
	230,324	*N*	2
	230,325	*N*	-
	231,464	*N*	-
	233,148	*N*	-
	234,874	*N*	-
	234,876	*N*	-
	235,287	*N*	-
	245,005	*N*	-
	245,006	*N*	-
	247,677	*N*	1
	255,747	*N*	2
Taiwan	AV 3905	*N*	1
	5154	*N*	1
	5156	*N*	1
	5157	*N*	1
	5158	*N*	1

*A.P. = Acid phosphatase zymogram pattern.

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1) Epistasis and soybean breeding

Epistasis, or non-allelic interaction, may be of considerable importance in the inheritance of quantitative traits in soybeans. Hanson and Weber (1962) and Hanson et al. (1967) used a nested progeny design to partition the genetic variance among homozygous lines into additive and additive x additive (epistatic) components. In each of two populations, approximately 70% of the genetic variance for grain yield was attributable to epistasis. While others (Leffel and Hanson, 1961; Brim and Cockerham, 1961) have given evidence for the predominance of additive variance for soybean yield, the implications for breeders of a large epistatic contribution to yield are worth considering.

A. Line selection. For line selection the reference population is taken to be a collection of homozygous lines extracted at random from a population

in linkage equilibrium. The genetic value of the lines can be fitted to the model $G = \mu + A + AA$, where μ is the population mean and A and AA represent deviations associated with additive and additive x additive effects, respectively. Higher order epistatic effects are assumed to be negligible. The variance among lines can be partitioned as $\sigma^2_G = \sigma^2_A + \sigma^2_{AA}$. It can be shown that the expected covariance between the genetic values of a parent and its pure-line offspring is $\frac{1}{2}\sigma^2_A + \frac{1}{4}\sigma^2_{AA}$, and that the regression of offspring on midparent genetic value is $1 - \frac{1}{2}K$, where $K = \sigma^2_{AA}/\sigma^2_G$, the proportion of the genetic variance attributable to epistasis.

For example, take K = 0.70, as in the studies of Hanson and Weber (1962) and Hanson et al. (1967). Then if two lines each yielding 10% above the population mean are crossed, lines derived from the cross will, in expectation, average 6.5%, not 10%, above the population mean. The results of crossing particular pairs of parents will deviate about this expected value.

In qualitative terms, selection among homozygous lines acts on both additive and epistatic components; a superior line is likely to have both *A* and *AA* positive. Less of the *AA* component than the *A* component is passed to progeny, however, because *A* effects are associated with alleles while *AA* effects are associated with allele combinations. Such combinations are subject to breakup through independent assortment and are not necessarily transmitted intact.

In the presence of additive x additive epistasis, line performance *per se* and parental value of lines (i.e., combining ability) are imperfectly correlated. There is both specific and general combining ability, neither of which is exactly predictable from line *per se* performance. It follows that a testcross procedure, such as that proposed by Kenworthy (1980), might be useful in eliminating poor parental material. Another testcross procedure is early generation testing, which could be used to select among crosses and enable greater testing effort to be given to the more promising crosses. The test material could be F_2-derived lines, bulk populations, or maturity-group bulks (Empig and Fehr, 1971).

B. Multi-parent crosses and intermated populations. Hanson et al. (1967) discussed the phenomenon of yield depression on intermating superior lines. The regression of offspring performance on parent mean when there are *n* parents is $1 - K(n-1)/n$. Thus, if K = 0.70, and if a ten-line synthetic is composed of lines averaging 10% above the reference population mean, lines

derived from the population are expected to average 3.7% above the reference population. The figure for a four-parent cross would be 4.75%. The number of generations of intermating has no effect on the amount of yield depression except where epistatic loci are linked.

Testcross selection could be used to identify parents that had good general combining ability and thus reduce the amount of depression that occurred with crossing or intermating.

C. Recurrent selection. Gains for recurrent selection for intrapopulation improvement derive chiefly from additive gene action. For selection among selfed families, the expected gain (ΔG) per cycle is the product of the standardized selection differential, i, and the additive portion of the genetic variance among families, divided by the phenotypic standard deviation (σ_p) of family means. Here it is assumed that dominance is absent and that the effective population size is so large that the epistatic contribution to genetic gain is negligible.

Under the model used by Hanson and Weber (1962), and Hanson et al. (1967), σ^2_A is defined as the additive genetic variance among homozygous lines. In general, the additive genetic variance among lines is $\frac{1}{2}(1+F)\sigma^2_A$, where F is the parental inbreeding coefficient (F = 0 for S_1 lines, $\frac{1}{2}$ for S_2 lines, 3/4 for S_3 lines, etc.).

The phenotypic variance among line means can be determined as

$$\sigma^2_P = \tfrac{1}{2}(1+F)\sigma^2_A + \tfrac{1}{4}(1+F)^2\sigma^2_{AA} + [\tfrac{1}{2}(1+F)\sigma^2_{AL} + \tfrac{1}{4}(1+F)^2\sigma^2_{AAL}]/L + \sigma^2_e/rL,$$

where σ^2_{AL}, σ^2_{AAL} and σ^2_e represent, respectively, the variance of additive genetic x location, additive x additive genetic x location, and interplot error effects, and where L and r are, respectively, the numbers of locations and replications per location.

The expected gain per cycle in recurrent selection is, therefore, $\Delta G = \frac{1}{2} i(1+F)\sigma^2_A/\sigma_p$. Epistasis contributes to the denominator, but not to the numerator, of this expression. Therefore, if epistasis is an important factor in the inheritance of a trait, estimates of genetic gain made by assuming all genetic variance to be additive will be biased upward.

Because the coefficients of the σ^2_{AA} and σ^2_{AAL} terms increase with inbreeding at a faster rate than those of the σ^2_A and σ^2_{AL} terms, the detrimental effect of epistasis on expected gain can be minimized by testing in the early generations.

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2) A new recurrent selection scheme incorporating genetic male sterility.

The use of genetic male sterility to facilitate recurrent selection in soybeans has been discussed by Brim and Stuber (1973), Fehr and Ortiz (1975), Kenworthy and Brim (1979) and Brim and Burton (1979). A problem with the selection schemes that have been presented is the occurrence of male-sterile segregates in the yield-test plots and the consequent reduction of precision in measuring yield. In the proposed scheme (Table 1), male sterility is employed to recombine selected lines, but tested material consists of homozygous fertile plants.

The main feature of the scheme is the inclusion of a seed-increase generation between the harvest of S_1 plants and the yield test. During this season, a homozygous fertile line is identified and increased for testing purposes, while a segregating-sterile bulk is made up using fertile plants from segregating rows derived from the same S_0 ancestor. This bulk represents the line in the recombination block.

The expected gain per cycle from this scheme is two-thirds that from ordinary S_2 testing, i.e., $(1/2)i\sigma_A^2/\sigma_p$, as compared with $(3/4)i\sigma_A^2/\sigma_p$ (see pages 104-107 for definitions of terms). The factor 2/3 represents parental control, in that the recombination makes use of relatives of superior lines rather than the lines themselves. The phenotypic standard deviation, σ_p, is the same as in ordinary S_2 testing (unless dominance is important). Aside from

Table 1

A new recurrent selection scheme incorporating genetic male sterility

Season	Activity
1	Grow intermating block in isolation. Harvest sterile (*ms ms*) plants.
2	Grow S_0 plants. Harvest fertile (*Ms ms*) plants.
3	Grow S_1 plants in progeny rows. Harvest 15 to 20 fertile plants (of which one-third will be *Ms Ms*, two-thirds *Ms ms*) from each row.
4	Grow S_2 plants in progeny rows. In each desirable S_0-derived family, (a) select one homozygous fertile row and bulk seed from it for testing, and (b) bulk seed from fertile (1/3 *Ms Ms*, 2/3 *Ms ms*) plants from the segregating rows. Seed from (b) provides material for the recombination should the line from (a) be selected on the basis of the yield test.
5	Conduct yield test of homozygous fertile S_2 lines (S_1-derived lines in the S_3). For the recombination in season 6, composite segregating bulks corresponding to the best fertile lines. This will give a recombination block segregating 5 fertile: 1 sterile.

decreased parental control, the proposed scheme has the additional disadvantages of increased cycle time (five seasons vs. four for ordinary S_2 testing) and increased labor and space in the breeder's nursery.

This procedure lends itself to several modifications, one of which consists of deferring testing by one generation, so that S_3 lines (S_2-derived lines in the S_4) are tested. In this modification, a heterozygous *Ms ms* S_1 plant is the ancestor of a homozygous fertile line to be tested and a segregating bulk to be recombined. Parental control is increased to 6/7 and expected gain becomes $(3/4)i\sigma_A^2/\sigma_p$ (where σ_p now refers to the phenotypic standard deviation among S_3 lines), compared to $(7/8)i\sigma_A^2/\sigma_p$ for ordinary S_3 testing.

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1) Pollination study on three varieties of soybeans using honeybees and leafcutter bees.

Soybeans are known to exhibit a high degree of flower abortion. Schaik and Probst (1958) noted that a large number of flowers open but drop off without ever forming pods. They also noted definite physical differences between shed ovules and viable ones. They stated that if flower shedding could be reduced or eliminated yield would most likely increase. Erickson et al. (1978), working with three soybean varieties obtained significantly higher yields (10-16%) in cages with honeybees (*Apis mellifera* L.) than in cages without bees for two of three varieties. We reasoned that some flowers might abort because they are never fertilized. Bees might increase the rate of fertilization by cross pollinating these flowers, thus, reduce abortion and increase yields.

We attempted to determine if honeybees and/or leafcutter bees could increase fertilization and reduce flower abortion. The experimental design used was a split-plot design with four replications. Whole plots were pollination treatments including a control with no cage and no bees, a cage with no bees, a cage with honey bees, and a cage with leafcutter bees. Sub-plot treatments included three varieties ('Crawford', 'Essex', and 'Forrest'). Planting date was June 3, 1980, and cages were erected over the designated plots on July 9, 1980 when the first plants began to flower. The cages and bees were left in the field until harvest on October 28, 1980.

Data were obtained on yield and yield components. Yield was recorded as grams/plot, and seed weight was recorded as grams/100 seeds. All plants within each plot were counted to determine plants/plot. Seeds/plant were determined indirectly.

There were no significant differences for yield or any yield component due to pollination treatments. Any differences which might have resulted from the treatments could have been masked by the adverse effects of extremely hot, dry conditions present during flowering and pod development. The negative results of this study do not rule out the possibility of inadequate fertilization as a factor involved in flower abortion. Further investigations are planned to determine if inadequate fertilization affects flower abortion.

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2) Hybridization of soybean parental line using the growth chamber.

We would like to make crosses for our breeding program in the growth chamber or greenhouse during the winter months. This will allow us to better utilize our time and personnel. It should also allow us to better match up parents in different maturity groups. Also, we can avoid field crossing which is difficult under the relatively dry, hot, windy conditions present in Oklahoma during the flowering season.

Wilcox (1974) reported that a 12-hour photoperiod resulted in early flowering and good seed production. According to Hammer (1969), the temperature should not be below 21°C nor above 32°C. During the past year, we have conducted several experiments in the growth chamber to determine the environmental conditions which are suitable for early flowering and artificial hybridization. Group V and VI varieties were grown in flats in the growth chamber. Each flat contained 6 rows with 20 plants/row. Rows were 38 cm long with 9 cm spacing between rows. Artificial lighting was provided by a mixture of cool white fluorescent and incandescent lights providing approximately 3,000 foot candles. Temperature was maintained at 26.7°C, and daylength was maintained at 12 hours. Varieties evaluated included 'Forrest', 'Essex', 'Mack', 'Bedford', 'York', 'Dare', 'Sohoma', 'Lee 74', 'Centennial', 'Gail', 'Lancer', and 'Davis'. The group V varieties all began to flower 37 days after planting. Plants were

approximately 15 cm in height. Group VI varieties began flowering from 37 to 41 days after planting. Flowers were small and most anthers dehisced before the flower could be effectively manipulated.

Reducing the temperature to 24°C after flowering began and increasing the humidity within the growth chamber appeared to produce a more satisfactory flower for artificial hybridization. The 3,000 foot candle light intensity and 12-hour photoperiod appear to be satisfactory. Reduced light intensity or reduced temperatures resulted in most varieties not flowering in a reasonably short time.

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1) Performance of lines from four generations of a backcrossing program involving *Glycine max* and *G. soja*.

We are interested in the possibility of using *Glycine soja* as a source of genes for improving cultivars of *Glycine max*. However, some characteristics in *G. soja*, such as low yield, vining, lodging, shattering, non-defoliation at maturity, poor seed quality, and non-yellow seed coat color are not acceptable in a cultivar. The purpose of our study is to explore the performance of these characters in lines derived from a backcrossing program in which *G. soja* is the donor parent.

Two *G. soja* introductions from the USSR, PI 424,001 and PI 326,581, were selected, based on complete fertility of the F_1 generation when crossed to cultivars of *G. max*. Two crosses were made, PI 424,001 x 'Amsoy 71' (Cross 1)

Table 1

Mean and genotypic variance of some agronomic characters in different generations of a backcrossing program involving *G. max* and *G. soja*

Cross		I. PI 424001 x Amsoy 71							
Generation		P_1 PI 424001	P_2 Amsoy 71	F_1 *	F_2	F_3	BC_1F_2	BC_2F_2	BC_3F_2
Number of families						235	39	39	39
Fraction of recurrent parent germplasm		0	1	0.5	0.5	0.5	0.75	0.875	0.9375
Lodging	$\bar{x}$	5.0	1.6	(5)	1-5	3.2	3.2	2.9	2.5
	$\hat{\sigma}_g^2$					1.35	0.45	0.16	0.23
Vining	$\bar{x}$	1	0	(1)	0-1	0.50	0.19	0.01	0
	$\hat{\sigma}_g^2$					0.16	0.07	0.006	0
Shattering at maturity	$\bar{x}$	1	0	(1)	0-1	0.50	0.14	0	0
	$\hat{\sigma}_g^2$					0.17	0.07	0	0
Shattering on October 31	$\bar{x}$	1	0	(1)	0-1	0.89	0.56	0.35	0.09
	$\hat{\sigma}_g^2$					0.07	0.12	0.09	0.03
Defoliation at maturity	$\bar{x}$	0	1	(1)	0-1	0.58	0.80	0.97	1
	$\hat{\sigma}_g^2$					0.18	0.11	0.03	0
Days to ** flowering	$\bar{x}$	30.0	41.5		32	35.9	38.2	39.8	40.6
	$\hat{\sigma}_g^2$					9.6	5.1	14.4	6.5
Days from first plant to half of plants flowering in a line **	$\bar{x}$	2.0	3.0		2	3.0	3.1	3.5	3.0
	$\hat{\sigma}_g^2$					2.4	2.8	4.4	1.0
Days to maturity	$\bar{x}$	85.0	118.0		107	107.9	113.5	115.6	117.2
	$\hat{\sigma}_g^2$					47.6	33.9	19.8	18.0
Days from first plant to half of plants mature in a line	$\bar{x}$	2.0	2.5		16	6.0	5.2	4.0	3.4
	$\hat{\sigma}_g^2$					5.7	4.3	4.6	2.6
Percentage of yellow seed coat (%)		0	100		12.3		48.6	61.8	74.5
Percentage of acceptable lines (%)						0.014	0.24	2.0	16.2

*F_1 was grown in the greenhouse, figures in parentheses are greenhouse value.

**Only 119 F_2-derived lines in F_3 observed

II. Century x PI 326581									
P_1 Century	P_2 PI 326581	F_1 *	F_2	F_3	BC_1F_2	BC_2F_2	BC_3F_2	5% L.S.D. ***	$\hat{\sigma}_e^2$
				241	43	43	43		
1	0	0.5	0.5	0.5	0.75	0.875	0.9375		
1.3	5	(5)	5	4.8 0.17	3.6 0.83	2.5 0.30	1.7 0.16	0.14	0.08
0	1	(1)	0-1	0.95 0.03	0.35 0.11	0 0	0 0	0	0
0	1	(1)	0-1	0.61 0.18	0.31 0.07	0 0	0 0	0	0
0	1	(1)	0-1	0.86 0.09	0.93 0.03	0.76 0.09	0.38 0.13	0	0
1	1	(1)	1	1† 0	1 0	1 0	1 0	0	0
40.0	66.0		48	51.0 136.8	40.2 21.3	38.4 6.2	38.5 2.6	0.3	0.25
2.0	2.0		14	7.2 30.6	4.7 11.6	2.9 2.8	2.5 1.0	0.3	0.33
119.0	113.0		121	120.9 52.6	117.0 22.7	116.0 12.6	116.5 6.4	0.3	0.33
				4.6 4.3	5.0 2.2	2.9 0.6	2.3 0	0.4	0.50
100	0		7		22.5	62.4	67.1		
				≃0	≃0	0.9	18.3		

***For comparisons between any two means of backcross generation.

†Thirty-three of 241 lines did not defoliate normally because of an early frost.

and 'Century' x PI 326,581 (Cross II), and three backcrosses were made to the *G. max* parent. The F_2 populations, F_2-derived lines in F_3, BC_1F_1-derived lines in BC_1F_2, BC_2F_1-derived lines in BC_2F_2, and BC_3F_1-derived lines in BC_3F_2 were grown in single 2 m rows without replication at Ames, Iowa in 1980. The parents were replicated four times in the field. Data were obtained for lodging score at maturity (1 = plants erect, 5 = plants prostrate); vining score (0 = no vining, 0.5 = intermediate vining or segregation, 1 = vining); shattering score (0 = no shattering, 0.5 = segregating, 1 = shattering) taken at maturity, on Oct. 15 (about 20 days after maturity) and on Oct. 31; defoliation score (0 = no defoliation at maturity, 0.5 = partial defoliation, 1 = defoliation); days from planting to flowering; days from planting to maturity; days from the time the first plant in a line flowered until 50% of the plants were in bloom; days from the time the first plant matured until 50% of the plants were mature; and seed coat color.

To obtain an estimate of the genotypic variance for each character, the variance among lines was used as the estimate of the phenotypic variance and the variance among four replications of each parent was used as environmental estimate.

As the percentage of the recurrent parent increased with backcrossing, the frequency of lines similar to the recurrent parent increased and the genetic variation decreased (Table 1). Two backcross generations were enough to avoid vining, non-defoliation at maturity, and shattering at maturity. For lodging score, shattering on Oct. 31, and yellow seed coat color, the mean of the lines after three backcrosses was not equal to the recurrent parent. Lodging score was significantly correlated with vining; the correlation coefficients were 0.64 and 0.66 in F_3 for Cross I and II, respectively. Yellow seed color was significantly correlated with light pod color; the values of chi-squares (χ^2) were 167.6 and 62.6 for Cross I and II, respectively ($\chi^2_{0.05} = 9.21$). If the selection criteria for the six characters are non-vining, non-shattering, normal defoliation at maturity, yellow seed coat, lodging score of 2 or less, and maturity from 'Hodgson 78' to 'Williams' (107 to 127 days after planting), we can estimate the percentage of superior lines in different backcross generations as shown in Table 1. The percentage of lines that met the six criteria was 0 to 0.2% in the BC_1, 0.9 to 2.0% in the BC_2, and 16.2 to 18.3% in the BC_3.

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1) Early maturing soybean mutant.

Breeding for earliness and tolerance to lower temperatures during vegetation period was a starting-point in expansion of soybean cultivation to the northern part of the world, characterized by long day conditions, lower temperatures and a short vegetation period (Holmberg, 1973).

Recently, the interest in soybean has increased and intensive breeding programs started in different countries of northern Europe, among them Poland.

Under Polish climatic conditions, most of soybean cultivars and forms from Maturity Group 00 are characterized by too long vegetation period and are very often killed by frost before maturation (Szyrmer, 1968). Taking into account this situation, breeding programs have been undertaken in order to get early soybean forms, which may be classified as Maturity Group 000.

The main emphasis in breeding for earliness has been laid on recombination breeding. However, there are few early introductions in the germplasm collection and the possibility of obtaining early soybean forms by mutation breeding (Zacharias, 1956; Kawai, 1970), a few soybean cultivars and forms were irradiated with gamma rays of ^{60}Co and were treated with N-methyl-N-nitroso urea (NMH).

Using gamma rays of ^{60}Co, air dried seeds were irradiated at the rate of 4, 7, 10, 13, 16, 19 kr. In the study with NMH, seeds were soaked in distilled water for 16 hr and then soaked in a mutagen solution at the concentration of 1, 1.5, 2 mM for 3 hr. The seeds were then washed in water and planted immediately.

Part of M_1 plants were harvested separately and seeds of each single plant were grown in individual rows. M_1 plants with a low number of seeds per plant were harvested in bulk and were planted up to M_3 generation using a modified single-seed-descent method. Selection of mutants were performed in both progeny-row and bulk populations starting from M_2 generations.

As a result of these operations, a lot of morphological as well as early maturing mutants have been obtained.

Table 1

Some agronomic characters of early maturing mutant line in comparison with parent and standard cultivars of soybean

Cultivar	Plant height cm			Number of seeds per plant			Weight of seeds per plant			Vegetation period		
	1979	1980	Mean	1979	1980	Mean	1979	1980	Mean	1979	1980	Mean
Ajma (Parent variety)	46.5	56.1	51.3	63.4	37.7	50.6	11.9	7.4	9.7	134	160	147
LA 1259/4 (Mutant line)	37.8	51.0	44.4	46.0	63.4	54.7	9.6	10.0	9.8	116	146	131
Fiskeby V (Check variety)	38.2	36.7	37.5	49.6	29.8	39.7	9.3	5.7	7.5	118	138	128
Mean for years	40.8	47.9		53.0	43.6		10.3	7.7		123	148	
L D S P = 0.05	3.0*		3.7*	8.2		10.1	1.4*		1.8			

*Differences significant at P = 0.01.

Table 1 presents some data concerning features of a mutant with short vegetation period selected from cultivar 'Ajma', comparing favorably with 'Fiskeby V', a variety with a proper vegetation period for Polish climatic conditions. The mutant has been derived from the combination 4 kr in M_3 generation and is homozygotic.

The weather conditions during growing seasons of two years of evaluation were different, moderate in 1979 and very unfavorable in 1980.

Sums of average daily temperatures for the growing seasons (from May to October) were, respectively, in 1979 - 2615°C, and in 1980 - 2406°C. The lower sum of average daily temperatures in 1980 (209°C) and the higher sum of precipitation (about 83 mm) than in 1979, caused a decrease of the number and weight of seeds per plant for Ajma and Fiskeby V and had an effect on duration of their vegetation period. There was a small difference of maturity time between the mutant line and Fiskeby V, but the mutant line had significantly higher plants, number and weight of seeds per plant (Table 1).

As can be noticed from Table 1, mutant LA 1259/4 had a 16-day-shorter vegetation period than Ajma, maintaining plants productivity at the same level as Ajma and higher, compared with Fiskeby V, which is one of the earliest ripening varieties in our climatic conditions. This mutant has shown small fluctuations of productivity for two years of trials.

Results of yield-testing experiment carried out in 1980 did not show marked differences of seeds yield among mutant line, Ajma and Fiskeby V. However, because of small plot size and number of replications, results obtained were treated as tentative and need confirmation.

In spite of that, unfavorable weather conditions indicate a possibility of selecting mutants that seem to be more tolerant to low temperatures and fit to our growing season. The best mutant lines will be evaluated in further experiments.

Example of mutant LA 1259/4 and others have shown the possibility of obtaining valuable mutants by means of mutation breeding. This technique may find application in breeding programs, particularly when early maturing selections in varieties with high yielding ability are desirable. However, finding early maturing mutants may be more difficult than finding late ones, although both types have been found (Gustafsson and Lundqvist, 1976) and the yielding ability as well as plant height of the most early maturing mutants are generally reduced.

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1) Observations and evaluation of *G. gracilis* and *G. soja* forms for crossing within the *Glycine* genus under climatic conditions in Poland.

Wild species of cultivated plants are well known to possess a high potential of adaptability manifested by high tolerance to unfavorable environmental conditions and to pathogens. They are often carriers of valuable biochemical properties. To have these properties transmitted to cultivated species would no doubt be advantageous from the point of view of agriculture. To this end, a thorough evaluation of wild forms should be made. At our Institute work was carried out on the variation range within the *Glycine max* species (Jaranowski et al., 1980) and on evaluation of wild forms of the *Soja* sub-genus for qualities valuable to genetic and breeding work under climatic conditions in Poland.

Materials: Seeds of *G. gracilis* and *G. soja* were kindly made available by Dr. R. Bernard, Urbana, Illinois, in 1975 and 1977, respectively. Samples of these two species were also received from the University of Morioko, Japan, in 1980. The batch of seeds from the Morioko University included 27 forms endemic to Japanese Islands, 18 from South Korea, two from Taiwan and one from the valley of the river Jangcy in China besides two forms, viz., PI 342,621A and PI 342,618, received from the Urbana Collection in the past. At

present, the number of plants totals 45 forms of *G. gracilis* and 111 forms of *G. soja* (Table 1).

Table 1

Number of *G. gracilis* and *G. soja* forms by origin

Country of origin	*G. gracilis*	*G. soja*
China	18	24
Japan	20	35
Korea	1	34
USSR	--	16
Taiwan	--	2
Other	6	--
Totals	45	111

Seeds of *G. gracilis* were grown in the field in 1975-1977 and in 1980 while those of *G. soja* were potted under greenhouse conditions and the pots left outside the house during the day. Attention was paid primarily to phenological phenomena, morphological traits and fertility.

Results: The process of vegetation of *G. gracilis* and *G. soja* forms. The geographical range of wild and semi-wild soybean forms is wide (30°N - 40°N). Our observations of the length of growing period point to considerable differences with country of origin.

In the field the forms of *G. gracilis* flowered between the second and third weeks of July. The first flowers were produced on the 9-10 node. The length of the flowering period varied with particular forms from 25 to 40 days. Start on harvest of *G. gracilis* was made at the end of September. The first to mature were two forms, one from Japan (PI 81,765) and one of unknown origin (PI 189,866). Around the mid of October ten other forms matured, including four from Japan, three from Manchuria, China. From the total of 45 *G. gracilis* forms gathered, seeds were collected from 28 (Table 2).

In the greenhouse, *G. soja* forms flowered earliest in the second week of July. The first to begin flowering were two forms from the region of Primorsk (43°N). In the third week of July three forms were observed to start flowering, originally grown on the river Amur in the region of Chabarovsk (48.5°N). In general, the common date of onset of flowering was

the first and second week of August. The length of flowering period ranged from 20 to 35 days. Harvesting was usually conducted from the third week of September to the middle of November. Seeds were collected from 39 forms. The number of *G. soja* forms maturing in Polish climatic conditions is presented by country of origin in Table 2. It appears from the Table that as many as 75% forms from China produced seeds, i.e., four from Manchuria (above 41°N), from the neighborhood of Harbin in the province Heilungkiang, nine from the province Kirin, and three from the neighborhood of Shenyang in the province Liaoning. Almost all *G. soja* forms from the provinces below 35°N failed to produce a single seed. Of this zone, only two forms matured, viz., from the provinces of Chantung and Kiangsu.

Table 2

Number of maturing forms of *G. gracilis* and *G. soja* by country of origin

Origin	*G. gracilis*			*G. soja*		
	No. of forms		% maturing forms	No. of forms		% maturing forms
	Collected	Maturing		Collected	Maturing	
China	18	13	72.2	24	18	75.0
Japan	20	9	45.0	35	4	11.4
South Korea	1	--	--	34	2	5.8
USSR	--	--	--	16	15	93.7
Taiwan	--	--	--	2	--	--
Other	6	6	100.0	--	--	--
Total	45	28	62.9	111	39	35.1

Forms of *G. soja* from the Soviet Union that reached maturity in Poland originated primarily from the region of Primorsk and Chabarovsk (43°N - 48.5°N). They included six forms from the region of Primorsk, four from the region of Vladivostok and three from the region of Chabarovsk. From the above zones, 93.7% forms matured (Table 2).

Of the large number of Japanese forms, only four matured in Poland (11.4%). Two of them were sampled in the neighborhood of Morioko (39.5°N) and two in

the Island of Hokkaido at Tokachi Plain. The remaining forms collected at lower latitudes initiated flowering late in September or did not set flowers at all. A similar response to long-day conditions was observed for *G. soja* forms from South Korea. Of the 34 forms collected, only two matured; they were from the neighborhood of Chunchon (39.5°N) (Table 2).

The two forms from Chabarovsk and Vladivostok, kindly supplied by Professor N. Kaizuna, were found to mature at the same time as their homologues received from Urbana. The forms from the valley of the river Jangcy (31°N) did not initiate flowering.

Morphology and yielding capacity of *G. gracilis* and *G. soja*: The *G. gracilis* plants of the examined population were more feeble than those of *G. max* and developed from 3 to 8 long branches. The plants were bushy, delicate and had thin light-brown hair on stems and leaves. Three of them were found to resemble the type of *G. max* plants. They had leaves longer than other forms of *G. gracilis*, dense hair and were of erect type. Two of them originated from Japan and one from Manchuria. The color of *G. gracilis* flowers was differentiated, from white to purple and dark violet. They grew closely together and generally formed five-flower-clusters or were observed in groups of two or three, settled at leaf axils. They varied in size. Nine forms produced relatively large flowers. Pods were smaller than in *G. max*, from light-brown to black in color, with 1-3 seeds per pod, averaged 2.2. The weight of 100 seeds was 5.7 g. From the maturing forms, approximately 36.0 seeds per plant were collected. Of the analyzed population, the Japanese form PI 81,765 matured earliest and produced the highest yield. Of interest from the breeding and genetic point of view were also other forms with satisfactory maturation and good yielding capacity, viz., PI 81,763, PI 81,768, PI 81,770 and PI 81,772 - all from Japan, besides the form PI 189,866 from an unidentified site.

The *G. soja* plants were characteristic of slender and feeble growth habit, with the height of the main stem reaching some 2.3 m at harvest. Flowers were small, from pink to violet. Pods were black and short. Exception to color were two light brown forms from the region of Primorsk (PI 342,619A and PI 342,619B). Seeds were small-sized, with the weight of 100 seeds approximating 1.9 g. The earliest forms set more than 50 pods per plant. The form PI 342,621C set generally 126 pods with 198 seeds and the PI 342,621B set 82 pods with 126 seeds. The two forms originated from the region of Amur,

Chabarovsk. Also, satisfactory maturation and good yielding capacity were noted for the form PI 342,621A from the same region and for three forms from the neighborhood of Primorsk, viz., PI 342,619A, PI 342,619B, and PI 342,622A.

Conclusions: (1) Of the 45 forms of *G. gracilis* and 111 forms of *G. soja* from various latitudes (30-40°N), 62.2% of *G. gracilis* plants matured in Poland (mostly from Manchuria) and 35.1% of *G. soja* (also from Manchuria, primarily from the provinces: Heilungkiang, Kirin, Liaoning and from the USSR, from Chabarovsk and Primorsk). (2) In the *G. gracilis* population the highest yield and earliest maturity was noted for five forms from Japan and one from an unidentified site. (3) In the population of *G. soja*, the earliest maturity and highest yields showed forms from the region of Chabarovsk and Primorsk.

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1) A report on induced mutations for soybean rust resistance*

Soybean is an important food legume in Thailand. Three recommended varieties, namely 'S.J.1', 'S.J.2' and 'S.J.4', are commonly used at present. These varieties are susceptible to rust, caused by *Phakopsora pachyrhizi* Syd., which is one of the serious soybean diseases in Thailand, especially when soybeans are planted in the wet season. Sources of resistant genes in existing germplasm collections were reported (Bromfield and Yang, 1976; Yang, 1977b). Some of these collections were tested in Thailand and were identified as either good to moderate tolerance (Pupipat, 1977) or susceptible (Nundhapun and Surin, 1977).

This paper reports a result on induced mutations for rust resistance in soybean by using gamma radiation.

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Approximately 10,000-23,000 seeds, with moisture content around 10%, from each of 11 cultivars, namely: 'G 8375', 'Wakashima' mutant #10, 'Taichung N', S.J. 2, S.J. 4, 'BM50', 'BM52', 'BM98', 'G 8377', 'G 8586', and 'G 8587', were irradiated in the Gammator at the Division of Radiation and Isotopes, Kasetsart University, with 15 and 30 krad, respectively; 1000 seeds of each cultivar were used for control.

The control and treated seeds were grown in July, 1979, at Farm Suwan, Pak Chong, Nakorn Rajchasima Province (latitude 14°30' N). Six pods were randomly harvested from each M_1 plant of all treatments at the end of October, 1979. M_2 seeds of each cultivar of different doses were bulked (M_2 bulk). In addition, 10 good M_1 plants from each treatment were selected and threshed singly (M_2 single).

Some part of M_2 bulk and seeds from M_2 single were planted at Mae Joe Experiment Station, Chiang Mai Province (latitude 18°30' - 19°N) in January, 1980, for rust evaluation. The natural rust disease incidence at Mae Joe Station in the dry season was not heavy enough for the effective rust screening. It was only possible to advance for another generation of M_2 bulk and M_2 single. M_2 plants of M_2 bulk populations and all rows of M_2 single were harvested in May, 1980. Both M_3 bulk and M_3 single seeds were planted in the rainy season of 1980 at two locations: Nong Hoi and Mae Joe Stations in Chiang Mai. In addition to M_3 bulk and M_3 single, seeds of remnant M_2 bulk also were planted at both stations in Chiang Mai for rust evaluation. The number of soybean rows planted at two locations in the rainy season, 1980, is shown in Table 1.

The natural rust disease incidence at Nong Hoi (altitude about 1,000 meters above the sea level) occurred and was severe enough for rust evaluation. Among 274 rows of M_2 and M_3 planted at Nong Hoi, it was observed in a single row (M_3 single) of Taichung N that among 39 soybean plants in the row, two plants showed the following rust reaction: The plants were still green, while the rest of them in the row were turning yellow. Based upon the IWGSR rating system (Yang, 1977a; Shanmugasundaram, 1977), these two plants showed similar rust reaction at different plant parts as 323, 233, 143 while the rest of the plants in that row were averaged 343. This observation was made 80 days after planting. At this time, the susceptible check-rows of TK5, as well as plants in control rows of Taichung N, S.J.2 and S.J.4, also averaged 343.

Table 1

Number of soybean rows (2.5 m - row) planted at two locations in the rainy season, 1980

	M_2 bulk		M_3 bulk		M_3 single		Total	
Cultivar	Nong Hoi	Mae Joe	Nong Hoi	Mae Joe	Nong Hoi	Mae Joe	Nong Hoi	Mae Joe
G 8375	9- 2C*	40- 4C	6- 1C	50- 1C	1- 1C	2- 1C	16- 4C	92- 6C
Wak. mut. #10	14- 2C	100- 4C	6- 1C	50- 5C	3- 1C	11- 1C	23- 4C	161- 10C
Taichung N	12- 2C	75- 4C	6- 1C	50- 5C	2- 1C	4- 2C	20- 4C	129- 11C
S.J.2	14- 2C	100- 4C	6- 1C	50- 5C	3- 1C	10- 2C	23- 4C	160- 11C
S.J.4	12- 2C	75- 4C	6- 1C	50- 5C	4- 1C	15- 2C	22- 4C	140- 11C
BM50	14- 2C	61- 4C	6- 1C	50- 5C	4- 1C	14- 2C	24- 4C	125- 11C
BM52	6- 2C	10- 4C	6- 1C	50- 5C	2- 1C	8- 0C	14- 4C	68- 9C
BM98	12- 2C	75- 4C	6- 1C	50- 5C	3- 1C	11- 3C	21- 4C	136- 12C
G 8377	14- 2C	100- 4C	6- 1C	50- 5C	4- 1C	16- 2C	24- 4C	166- 11C
G 8586	14- 2C	100- 4C	6- 1C	50- 5C	3- 1C	15- 2C	23- 4C	165- 11C
G 8587	13- 2C	90- 4C	6- 1C	50- 5C	1- 1C	2- 1C	20- 4C	142- 10C
Total	134-22C	826-44C	66-11C	550-51C	30-11C	108-18C	230-44C	1484-113C

*C = control rows.

According to this rating system, these two plants may have some resistance. The soybean plants of this type from other cultivars in this experiment at both locations are to be tagged and selected for further studies.

Among 11 cultivars used in this experiment, Taichung N shows some interesting rust reaction. This Taichung N was derived from the M_3 plants selected at Pak Chong in 1977 (Smutkupt et al., 1978).

For this reason, some Taichung N seeds will be reirradiated and evaluated for rust resistance in the rainy season of 1981.

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1) Effect of nutrient foliar application and seeding rate on promising soybean (*Glycine max*, Merrill) varieties in Mekong Delta, Vietnam.

In order to boost grain yield of soybeans by cultural practices, an experiment was carried out with two most promising soybean varieties in Mekong Delta, VN.

The experimental design is split plot design with three replicates. Plot size is 6.5m x 2m, with and/or without nutrient foliar spraying in main plots, and seeding rate is in subplots with four different seeding treatments: 40 x 20 cm, 40 x 5 cm, 30 x 10 cm and 30 x 5 cm that is, from 25 plants per square meter to 66 plants per square meter. Chemical fertilizers are applied with formula 40-60-60 KgN, P_2O_5, and K_2O per hectare as basic fertilizer application. Foliar spray is 40- 4- 12- 2 kg N, P_2O_5, K_2O and S per hectare in proportion of 10- 9- 3 and 0.5, applied in 9 times from 21 to 69 days after planting.

Results and discussion

a) Plant height: Seeding rate exerts a drastic effect on plant height at maturing stage. Plant height of soybean variety WRS No. 6 (a local soybean variety) differs from 18.6 to 21.7 and that of soybean variety WRS No. 4 (a selected soybean variety from Japan) differs from 47 to 62 cm. Seeding rate is positively proportional with plant height, but nutrient foliar spray does not have any effect on plant height.

b) Grain yield and yield components: Number of pods and number of seeds per square meter are both significantly different at 1% level. From 25 to 66 plants per square meter, seeding rate gives an increase of pods from 679 to 1449 pods/sq m in WRS No. 4 soybean variety and from 1196 to 1538 pods/sq m in WRS No. 6 soybean variety. Number of seeds per square meter also differs from 1261 to 2835 seeds/sq m in soybean variety WRS No. 4 and from 2365 to 3093 seeds/sq m in soybean variety WRS No. 6. Foliar spray gives an insignificant increase of both pods and/or seeds per square meter.

100-seed weight does not significantly differ in soybean variety WRS No. 6, but inversely, it does differ in soybean variety WRS No. 4 from 19.7 to 33.8 gr/100 seeds. Due to seeding rate, grain yield significantly differs at 1% level in both soybean varieties tested.

Table 1

Effect of nutrient foliar spray and seeding rate on grain yield of promising soybean varieties in Mekong Delta, Vietnam

No. of plants per sq. m	Soybean variety					
	WRS No. 4			WRS No. 6		
	So*	S1*	Mean	So	S1	Mean
66	5.49	5.80	5.64	4.35	4.52	4.43
50	4.65	5.05	4.85	3.85	4.14	3.98
33	3.50	4.10	3.80	3.68	3.87	3.77
25	3.04	2.99	3.01	3.45	3.54	3.49
At 5% level			0.33			0.42
At 1% level			0.46			0.60
C. V. %			9.14			8.66

*So means without foliar spray; S1 with foliar spray.

Table 2

Agronomic characters of two most promising soybean varieties in Mekong Delta, Vietnam

Variety	Days to maturing	Days to flowering	Color of pubescence	Color of flower	Plant height (cm)	No. of pods/ plant	100-seed/ weight (g)
WRS No. 4	90-100	28-29	white	white	20-30	20-30	over 20
WRS No. 6	85- 90	30	white	purple	40-60	30-50	13-15

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1) Reaction to peanut mottle virus in plant introductions of Maturity Groups 00 through IV.

The results of screening the soybean plant introductions in Maturity Groups II, III, and IV have been reported by Shipe et al. (1979). The results of evaluating the earlier maturity groups are reported here. Plant introductions that became available after 1976 have not been screened.

Materials and methods. The strains of peanut mottle virus (PMV) used were derived from the strain used in the previous screenings and produce similar reactions. The same inoculation methods were used.

All of the Maturity Group 00 and 0 plant introductions were evaluated in the greenhouse in 1978 and 1979, respectively. In Maturity Group I, FC 03,609 through PI 189,916 were evaluated in the greenhouse and PI 189,917 through PI 391,589A were evaluated in the field at Blacksburg. Germination was poor for some lines, so only one or two plants were available for inoculations. However, 5 to 15 plants from most lines were evaluated in the greenhouse and 15 to 30 plants in the field. Table 1 shows the plant introductions evaluated in each maturity group and those which were not evaluated because they either were missing or did not germinate.

Results. It appears that none of the plant introductions in Maturity Groups 00, 0 and I are resistant to PMV. Symptom expression varied somewhat, but none were found which were free of symptoms. A few lines, of which only one or two plants were available, did not exhibit symptoms, but it is believed they were escapes. Those lines include PI 153,237 and PI 361,121 of Group 0 and PI 86,410, PI 291,320A, PI 339,868A and PI 342,437 of Group I.

Twelve lines in Group I were observed to exhibit very mild symptoms in comparison to most other lines. Those included PI numbers 248,400, 253,658C, 291,281, 361,062A, 361,065A, 361,066A, 361,066B, 361,088A, 361,088B, 361,095, 361,098, and 361,117.

Discussion. When the results from screening the plant introductions in Maturity Groups 00 through IV are compared (Table 2), it is apparent that the frequency of resistant lines becomes successively higher in the later maturity groups. This association was noted by Shipe et al. (1979) and was assumed to

Table 1

Soybean plant introductions evaluated for reaction to PMV

Maturity Group	Highest PI no. tested	Total lines tested	PI lines not tested	
00	384,467	210	189932	
			194641	
			196502	
			196530	
0	399,074	279	FC21340	290122
			70242-4	290139
			153239	290144
			153240	297520
			153242	297522
			161989	361111
			227565	
I	391,589A	301	69507	86737
			70017	181536
			79610	196160
			79699	205085
			81033	297523
			83945-3	372404A
			86021	391583
			86133	

Table 2

Summary of frequency of plant introductions classified as resistant in Maturity Groups 00-IV

Maturity Group	Lines classed resistant	
	No.	% of total tested
00	0	0
0	0	0
I	0	0
II	7	1.3
III	16	2.5
IV	122	12.7

be either an artifact or evidence for co-evolution of the two organisms. The addition of the data for the three early maturity groups and additional verification of the data of Shipe et al. (unpublished) tend to favor the co-evolution hypothesis.

Bock and Kuhn (1975) reported the geographical distribution of PMV as southeast United States, East Africa, northeast Australia and probably Japan, West Malaysia, Venezuela and Bulgaria. These areas are largely at lower latitudes and all are within 40° of the equator. Group 00 to I soybeans are adapted outside of those limits. Assuming that the evaluated plant introductions are representative samples of the soybeans grown in their areas of adaptation, one might hypothesize some sort of association between the distribution of PMV and of lines resistant to the virus. Co-evolution is perhaps the simplest hypothesis, but more information is needed for proof. Genetic associations of PMV resistance with adaptation to specific latitudes or climates could cause similar distributions in the absence of PMV. Also, the close linkage between genes conferring resistance to PMV and soybean mosaic virus reported by Roane et al. (1980) could play a part. Unfortunately, our data don't provide much guidance as to the cause of the observed association, but the large number of lines included in the samples makes it appear to be more than a coincidence. More information on the representativeness of the germplasm collection, on the frequency of PMV resistance in later maturity groups and on the historical development of the various maturity groups might be helpful in verifying and explaining the apparent association of PMV resistance with maturity.

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